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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁵ : A61K 37/02, A01N 1/02	A1	(11) International Publication Number: WO 93/04692 (43) International Publication Date: 18 March 1993 (18.03.93)
(21) International Application Number: PCT/US92/07358 (22) International Filing Date: 28 August 1992 (28.08.92) (30) Priority data: 752,764 30 August 1991 (30.08.91) US 752,861 30 August 1991 (30.08.91) US 753,059 30 August 1991 (30.08.91) US (71) Applicant: CREATIVE BIOMOLECULES, INC. [US/ US]; 35 South Street, Hopkinton, MA 01748 (US). (72) Inventors: KUBERASAMPATH, Thangavel ; 6 Spring Street, Medway, MA 02053 (US). PANG, Roy, H., L. ; 15 Partridge Road, Etna, NH 03750 (US). OPPER- MANN, Hermann ; 25 Summer Hill Road, Medway, MA 02053 (US). RUEGER, David, C. ; 19 Downey Street, Hopkinton, MA 01748 (US). COHEN, Charles, M. ; 98 Winthrop Street, Medway, MA 02053 (US). OZ- KAYNAK, Engin ; 44 Purdue Drive, Milford, MA 01757 (US). SMART, John, E. ; 50 Meadow Brook Road, Weston, MA 02193 (US).		(74) Agents: KELLEY, Robin, D.; Testa, Hurwitz & Thibault, Exchange Place, 53 State Street, (US) et al. (81) Designated States: AU, CA, JP, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, SE). Published <i>With international search report.</i> <i>With amended claims.</i>
(54) Title: MORPHOGEN-INDUCED MODULATION OF INFLAMMATORY RESPONSE (57) Abstract The present invention is directed to methods and compositions for alleviating tissue destructive effects associated with the inflammatory response to tissue injury in a mammal. The methods and compositions include administering a therapeutically effective concentration of a morphogen or morphogen-stimulating agent sufficient to alleviate immune cell-mediated tissue destruction.		

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**MORPHOGEN-INDUCED MODULATION OF
INFLAMMATORY RESPONSE**

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Field of the Invention

10 The present invention relates generally to a method
for modulating the inflammatory response induced in a
mammal following tissue injury. More particularly,
this invention relates to a method for alleviating
immune-cell mediated tissue destruction associated with
15 the inflammatory response.

Background of the Invention

 The body's inflammatory response to tissue injury
20 can cause significant tissue destruction, leading to
loss of tissue function. Damage to cells resulting
from the effects of inflammatory response e.g., by
immune-cell mediated tissue destruction, has been
implicated as the cause of reduced tissue function or
25 loss of tissue function in diseases of the joints
(e.g., rheumatoid and osteo-arthritis) and of many
organs, including the kidney, pancreas, skin, lung and
heart. For example, glomerular nephritis, diabetes,
inflammatory bowel disease, vascular diseases such as
30 atherosclerosis and vasculitis, and skin diseases such
as psoriasis and dermatitis are believed to result in
large part from unwanted acute inflammatory reaction
and fibrosis. A number of these diseases, including
arthritis, psoriasis and inflammatory bowel disease are
35 considered to be chronic inflammatory diseases. The

damaged tissue also often is replaced by fibrotic tissue, e.g., scar tissue, which further reduces tissue function. Graft and transplanted organ rejection also is believed to be primarily due to the action of the
5 body's immune/inflammatory response system.

The immune-cell mediated tissue destruction often follows an initial tissue injury or insult. The secondary damage, resulting from the inflammatory
10 response, often is the source of significant tissue damage. Among the factors thought to mediate these damaging effects are those associated with modulating the body's inflammatory response following tissue injury, e.g., cytokines such as interleukin-1 (IL-1)
15 and tumor necrosis factor (TNF), and oxygen-derived free radicals such as superoxide anions. These humoral agents are produced by adhering neutrophilic leukocytes or by endothelial cells and have been identified at ischemic sites upon reperfusion. Moreover, TNF
20 concentrations are increased in humans after myocardial infarction.

A variety of lung diseases are characterized by airway inflammation, including chronic bronchitis,
25 emphysema, idiopathic pulmonary fibrosis and asthma. Another type of lung-related inflammation disorders are inflammatory diseases characterized by a generalized, wide-spread acute inflammatory response such as adult respiratory distress syndrome. Another dysfunction
30 associated with the inflammatory response is that mounted in response to injury caused by hyperoxia, e.g., prolonged exposure to lethally high concentrations of O_2 (95-100% O_2). Similarly, reduced

blood flow to a tissue (and, therefore reduced or lack of oxygen to tissues), as described below, also can induce a primary tissue injury that stimulates the inflammatory response.

5

It is well known that damage occurs to cells in mammals which have been deprived of oxygen. In fact, the interruption of blood flow, whether partial (hypoxia) or complete (ischemia) and the ensuing inflammatory responses may be the most important cause of coagulative necrosis or cell death in human disease. The complications of atherosclerosis, for example, are generally the result of ischemic cell injury in the brain, heart, small intestines, kidneys, and lower extremities. Highly differentiated cells, such as the proximal tubular cells of the kidney, cardiac myocytes, and the neurons of the central nervous system, all depend on aerobic respiration to produce ATP, the energy necessary to carry out their specialized functions. When ischemia limits the oxygen supply and ATP is depleted, the affected cells may become irreversibly injured. The ensuing inflammatory responses to this initial injury provide additional insult to the affected tissue. Examples of such hypoxia or ischemia are the partial or total loss of blood supply to the body as a whole, an organ within the body, or a region within an organ, such as occurs in cardiac arrest, pulmonary embolus, renal artery occlusion, coronary occlusion or occlusive stroke.

30

The tissue damage associated with ischemia-reperfusion injury is believed to comprise both the initial cell damage induced by the deprivation of oxygen to the cell and its subsequent recirculation, as well as the damage caused by the body's response to

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this initial damage. It is thought that reperfusion injury may result in dysfunction to the endothelium of the vasculature as well as injury to the surrounding tissue. In idiopathic pulmonary fibrosis, for example, 5 scar tissue accumulates on the lung tissue lining, inhibiting the tissue's elasticity. The tissue damage associated with hyperoxia injury is believed to follow a similar mechanism, where the initial damage is mediated primarily through the presence of toxic oxygen 10 metabolites followed by an inflammatory response to this initial injury.

Similarly, tissues and organs for transplantation also are subject to the tissue destructive effects 15 associated with the recipient host body's inflammatory response following transplantation. It is currently believed that the initial destructive response is due in large part to reperfusion injury to the transplanted organ after it has been transplanted to the organ 20 recipient.

Accordingly, the success of organ or tissue transplantation depends greatly on the preservation of the tissue activity (e.g., tissue or organ viability) 25 at the harvest of the organ, during storage of the harvested organ, and at transplantation. To date, preservation of organs such as lungs, pancreas, heart and liver remains a significant stumbling block to the successful transplantation of these organs. U.S. 30 Patent No. 4,952,409 describes a superoxide dismutase-containing liposome to inhibit reperfusion injury. U.S. Patent No. 5,002,965 describes the use of ginkgolides, known platelet activating factor antagonists, to inhibit reperfusion injury. Both of 35 these factors are described working primarily by

inhibiting the release of and/or inhibiting the
damaging effects of free oxygen radicals. A number of
patents also have issued on the use of
immunosuppressants for inhibiting graft rejection. A
representative listing includes U.S. Patent Nos.
5,104,858, 5,008,246 and 5,068,323. A significant
problem with many immunosuppressants is their low
therapeutic index, requiring the administration of high
doses that can have significant toxic side effects.

10

Rheumatoid and osteoarthritis are prevalent
diseases characterized by chronic inflammation of the
synovial membrane lining the afflicted joint. A major
consequence of chronic inflammatory joint disease
(e.g., rheumatoid arthritis) and degenerative arthritis
(e.g., osteoarthritis) is loss of function of those
affected joints. This loss of function is due
primarily to destruction of the major structural
components of the joint, cartilage and bone, and
subsequent loss of the proper joint anatomy. As a
consequence of chronic disease, joint destruction
ensues and can lead to irreversible and permanent
damage to the joint and loss of function. Current
treatment methods for severe cases of rheumatoid
arthritis typically include the removal of the synovial
membrane, e.g., synovectomy. Surgical synovectomy has
many limitations, including the risk of the surgical
procedure itself, and the fact that a surgeon often
cannot remove all of the diseased membrane. The
diseased tissue remaining typically regenerates,
causing the same symptoms which the surgery was meant
to alleviate.

30

Psoriasis is a chronic, recurrent, scaling skin disease of unknown etiology characterized by chronic inflammation of the skin. Erythematous eruptions, often in papules or plaques, and usually having a white silvery scale, can affect any part of the skin, but most commonly affect the scalp, elbows, knees and lower back. The disease usually occurs in adults, but children may also be affected. Patients with psoriasis have a much greater incidence of arthritis (psoraitic arthritis), and generalized exfoliation and even death can threaten afflicted individuals.

Current therapeutic regimens include topical or intralesional application of corticosteroids, topical administration of keratolytics, and use of tar and UV light on affected areas. No single therapy is ideal, and it is rare for a patient not to be treated with several alternatives during the relapsing and remitting course of the disease. Whereas systematic treatment can induce prompt resolution of psoriatic lesions, suppression often requires ever-increasing doses, sometimes with toxic side effect, and tapering of therapy may result in rebound phenomena with extensions of lesions, possibly to exfoliation.

Inflammatory bowel disease (IBD) describes a class of clinical disorders of the gastrointestinal mucosa characterized by chronic inflammation and severe ulceration of the mucosa. The two major diseases in this classification are ulcerative colitis and regional enteritis (Crohn's Disease). Like oral mucositis, the diseases classified as IBD are associated with severe mucosal ulceration (frequently penetrating the wall of the bowel and forming strictures and fistulas), severe mucosal and submucosal inflammation and edema, and

fibrosis (.g., scar tissue f rmation which interferes with the acid protective function of the gastrointestinal lining.) Other forms of IBD include regional ileitis and proctitis. Clinically, patients with fulminant IBD can be severely ill with massive diarrhea, blood loss, dehydration, weight loss and fever. The prognosis of the disease is not good and frequently requires resection of the diseased tissue.

Therefore, an object of the present invention is to provide a method for protecting mammalian tissue, particularly human tissue, from the damage associated with the inflammatory response following a tissue injury. The inflammatory reaction may be in response to an initial tissue injury or insult. The original injury may be chemically, mechanically, biologically or immunologically related. Another object is to provide methods and compositions for protecting tissue from the tissue destructive effects associated with chronic inflammatory diseases, including arthritis (e.g., rheumatoid or osteoarthritis), psoriatic arthritis, psoriasis and dermatitis, inflammatory bowel disease and other autoimmune diseases. Yet another object is to provide methods and compositions for enhancing the viability of mammalian tissues and organs to be transplanted, including protecting the transplanted organs from immune cell-mediated tissue destruction, such as the tissue damage associated with ischemia-reperfusion injury. This tissue damage may occur during donor tissue or organ harvesting and transport, as well as following initiation of blood flow after transplantation of the organ or tissue in the recipient host.

Another object of the invention is to provide a method for alleviating tissue damage associated with ischemic-reperfusion injury in a mammal following a deprivation of oxygen to a tissue in the mammal. Other
5 objects of the present invention include providing a method for alleviating tissue damage associated with ischemic-reperfusion injury in a human which has suffered from hypoxia or ischemia following cardiac
10 arrest, pulmonary embolus, renal artery occlusion, coronary occlusion or occlusive stroke. A further object is to provide a method for alleviating tissue damage associated with hyperoxia-induced tissue injury, e.g., lethally high oxygen concentrations.

15 Still another object of the invention is to provide a method for modulating inflammatory responses in general, particularly those induced in a human following tissue injury.

20 These and other objects and features of the invention will be apparent from the description, drawings and claims which follow.

Summary of the Invention

The present invention provides a method for alleviating the tissue destructive effects associated with activation of the inflammatory response following tissue injury. The method comprises the step of providing to the affected tissue a therapeutically effective concentration of a morphogenic protein ("morphogen", as defined herein) upon tissue injury or in anticipation of tissue injury, sufficient to substantially inhibit or reduce the tissue destructive effects of the inflammatory response.

In one aspect, the invention features compositions and therapeutic treatment methods that comprise the step of administering to a mammal a therapeutically effective amount of a morphogenic protein ("morphogen"), as defined herein, upon injury to a tissue, or in anticipation of such injury, for a time and at a concentration sufficient to inhibit the tissue destructive effects associated with the body's inflammatory response, including repairing damaged tissue, and/or inhibiting additional damage thereto.

In another aspect, the invention features compositions and therapeutic treatment methods for protecting tissues and organs from the tissue destructive effects of the inflammatory response which include administering to the mammal, upon injury to a tissue or in anticipation of such injury, a compound that stimulates in vivo a therapeutically effective concentration of an endogenous morphogen within the body of the mammal sufficient to protect the tissue from the tissue destructive effects associated with the inflammatory response, including repairing damaged

tissu and/or inhibiting additional damage theret .
These compounds are referred to herein as morphogen-
stimulating agents, and are understood to include
substances which, when administered to a mammal, act on
5 cells of tissue(s) or organ(s) that normally are
responsible for, or capable of, producing a morphogen
and/or secreting a morphogen, and which cause the
endogenous level of the morphogen to be altered. The
agent may act, for example, by stimulating expression
10 and/or secretion of an endogenous morphogen.

As embodied herein, the term "ischemic-reperfusion
injury" refers to the initial damage associated with
oxygen deprivation of a cell and the subsequent damage
15 associated with the inflammatory response when the cell
is resupplied with oxygen. As embodied herein, the
term "hyperoxia-induced injury" refers to the tissue
damage associated with prolonged exposure to lethally
high doses of oxygen, e.g., greater than 95% O₂,
20 including the tissue damage associated with the
inflammatory response to the toxically high oxygen
dose. Accordingly, as used herein, "toxic oxygen
concentrations" refers to the tissue damage associated
with the injury induced by both lethally low oxygen
25 concentrations of oxygen (including a complete lack of
oxygen), and by lethally high oxygen concentrations.
The expression "alleviating" means the protection from,
reduction of and/or elimination of undesired tissue
destruction, particularly immune cell-mediated tissue
30 destruction. The tissue destruction may be in response
to an initial tissue injury, which may be mechanical,
chemical or immunological in origin. The expression
"enhance the viability of" living tissues or organs, as
used herein, means protection from, reduction of and/or
35 elimination of reduced or lost tissue or organ function

as a result of tissue death, particularly immune cell-mediated tissue death. "Transplanted" living tissue encompasses both tissue transplants (e.g., as in the case of bone marrow transplants) and tissue grafts.

5 Finally, a "free oxygen radical inhibiting agent" means a molecule capable of inhibiting the release of and/or inhibiting tissue damaging effects of free oxygen radicals.

10 In one embodiment of the invention, the invention provides methods and compositions for alleviating the ischemic-reperfusion injury in mammalian tissue resulting from a deprivation of, and subsequent reperfusion of, oxygen to the tissue. In another
15 embodiment, the invention provides a method for alleviating the tissue-destructive effects associated with hyperoxia. In still another embodiment of the invention, the invention provides methods and compositions for maintaining the viability of tissues
20 and organs, particularly living tissues and organs to be transplanted, including protecting them from ischemia-reperfusion injury. In still another embodiment, the invention provides methods for protecting tissues and organs from the tissue
25 destructive effects of chronic inflammatory diseases, such as arthritis, psoriasis, dermatitis, including contact dermatitis, IBD and other chronic inflammatory diseases of the gastrointestinal tract, as well as the tissue destructive effects associated with other, known
30 autoimmune diseases, such as diabetes, multiple sclerosis, amyotrophic lateral sclerosis (ALS), and other autoimmune neurodegenerative diseases.

In one aspect of the invention, the morphogen is provided to the damaged tissue following an initial injury to the tissue. The morphogen may be provided directly to the tissue, as by injection to the damaged tissue site or by topical administration, or may be provided indirectly, e.g., systemically by oral or parenteral means. Alternatively, as described above, an agent capable of stimulating endogenous morphogen expression and/or secretion may be administered to the mammal. Preferably, the agent can stimulate an endogenous morphogen in cells associated with the damaged tissue. Alternatively, morphogen expression and/or secretion may be stimulated in a distant tissue and the morphogen transported to the damaged tissue by the circulatory system.

In another aspect of the invention, the morphogen is provided to tissue at risk of damage due to immune cell-mediated tissue destruction. Examples of such tissues include tissue grafts and tissue or organ transplants, as well as any tissue or organ about to undergo a surgical procedure or other clinical procedure likely to either inhibit blood flow to the tissue or otherwise induce an inflammatory response. Here the morphogen or morphogen-stimulating agent preferably is provided to the patient prior to induction of the injury, e.g., as a prophylactic, to provide a cyto-protective effect to the tissue at risk.

Where the tissue at risk comprises a tissue or organ to be transplanted, the tissue or organ to be transplanted preferably is exposed to a morphogen prior to transplantation. Most preferably, the tissue or organ is exposed to the morphogen prior to its removal from the donor, by providing the donor with a

composition comprising a morphogen or morphogen-stimulating agent. Alternatively or, in addition, once removed from the donor, the organ or tissue is placed in a preservation solution containing a morphogen or morphogen-stimulating agent. In addition, the recipient also preferably is provided with a morphogen or morphogen-stimulating agent just prior to, or concomitant with, transplantation. In all cases, the morphogen or morphogen-stimulating agent may be administered directly to the tissue at risk, as by injection or topical administration to the tissue, or it may be provided systemically, either by oral or parenteral administration.

The morphogens described herein are envisioned to be useful in enhancing viability of any organ or living tissue to be transplanted. The morphogens may be used to particular advantage in lung, heart, liver, kidney or pancreas transplants, as well as in transplantation and/or grafting of bone marrow, skin, gastrointestinal mucosa, and other living tissues.

Where the patient suffers from a chronic inflammatory disease, such as diabetes, arthritis, psoriasis, IBD, and the like, the morphogen or morphogen-stimulating agent preferably is administered at regular intervals as a prophylactic, to prevent and/or inhibit the tissue damage normally associated with the disease during flare periods. As above, the morphogen or morphogen-stimulating agent may be provided directly to the tissue at risk, for example by injection or by topical administration, or indirectly, as by systemic e.g., oral or parenteral administration.

Among the morphogens useful in this invention are proteins originally identified as osteogenic proteins, such as the OP-1, OP-2 and CBMP2 proteins, as well as amino acid sequence-related proteins such as DPP (from *Drosophila*), Vgl (from *Xenopus*), Vgr-1 (from mouse, see U.S. 5,011,691 to Oppermann et al.), GDF-1 (from mouse, see Lee (1991) PNAS 88:4250-4254), all of which are presented in Table II and Seq. ID Nos. 5-14), and the recently identified 60A protein (from *Drosophila*, Seq. ID No. 24, see Wharton et al. (1991) PNAS 88:9214-9218.) The members of this family, which include members of the TGF- β super-family of proteins, share substantial amino acid sequence homology in their C-terminal regions. The proteins are translated as a precursor, having an N-terminal signal peptide sequence, typically less than about 30 residues, followed by a "pro" domain that is cleaved to yield the mature sequence. The signal peptide is cleaved rapidly upon translation, at a cleavage site that can be predicted in a given sequence using the method of Von Heijne ((1986) Nucleic Acids Research 14:4683-4691.) Table I, below, describes the various morphogens identified to date, including their nomenclature as used herein, their Seq. ID references, and publication sources for the amino acid sequences for the full length proteins not included in the Seq. Listing. The disclosure of these publications is incorporated herein by reference.

TABLE I

30	"OP-1"	Refers generically to the group of morphogenically active proteins expressed from part or all of a DNA sequence encoding OP-1 protein, including allelic and species variants thereof, e.g., human
35		

OP-1 ("hOP-1", Seq. ID No. 5, mature protein amino acid sequence), or mouse OP-1 ("mOP-1", Seq. ID No. 6, mature protein amino acid sequence.) The conserved seven cysteine skeleton is defined by residues 38 to 139 of Seq. ID Nos. 5 and 6. The cDNA sequences and the amino acids encoding the full length proteins are provided in Seq. ID Nos. 16 and 17 (hOP1) and Seq. ID Nos. 18 and 19 (mOP1.) The mature proteins are defined by residues 293-431 (hOP1) and 292-430 (mOP1). The "pro" regions of the proteins, cleaved to yield the mature, morphogenically active proteins are defined essentially by residues 30-292 (hOP1) and residues 30-291 (mOP1).

"OP-2" refers generically to the group of active proteins expressed from part or all of a DNA sequence encoding OP-2 protein, including allelic and species variants thereof, e.g., human OP-2 ("hOP-2", Seq. ID No. 7, mature protein amino acid sequence) or mouse OP-2 ("mOP-2", Seq. ID No. 8, mature protein amino acid sequence). The conserved seven cysteine skeleton is defined by residues 38 to 139 of Seq. ID Nos. 7 and 8. The cDNA sequences and the amino acids encoding the full length proteins are provided in Seq. ID Nos. 20 and 21 (hOP2) and Seq. ID Nos. 22 and 23 (mOP2.) The mature proteins are defined essentially by residues 264-402 (hOP2) and 261-399 (mOP2). The "pro"

regions of the proteins, cleaved to yield the mature, morphogenically active proteins likely are defined essentially by residues 18-263 (hOP2) and residues 18-260 (mOP2). (Another cleavage site also occurs 21 residues upstream for both OP-2 proteins.)

5
10 "CBMP2" refers generically to the morphogenically active proteins expressed from a DNA sequence encoding the CBMP2 proteins, including allelic and species variants thereof, e.g., human CBMP2A ("CBMP2A(fx)", Seq ID No. 9) or human CBMP2B DNA ("CBMP2B(fx)", Seq. ID No. 10). The amino acid sequence for the full length proteins, referred to in the literature as BMP2A and BMP2B, or BMP2 and BMP4, appear in Wozney, et al. (1988) Science 242:1528-1534. The pro domain for BMP2 (BMP2A) likely includes residues 25-248 or 25-282; the mature protein, residues 249-396 or 283-396. The pro domain for BMP4 (BMP2B) likely includes residues 25-256 or 25-292; the mature protein, residues 257-408 or 293-408.

25
30 "DPP(fx)" refers to protein sequences encoded by the Drosophila DPP gene and defining the conserved seven cysteine skeleton (Seq. ID No. 11). The amino acid sequence for the full length protein appears in Padgett, et

al (1987) Nature 325: 81-84. The pro domain likely extends from the signal peptide cleavage site to residue 456; the mature protein likely is defined by residues 457-588.

5 "Vgl(fx)" refers to protein sequences encoded by the Xenopus Vgl gene and defining the conserved seven cysteine skeleton (Seq. ID No. 12). The amino acid sequence for the full length protein appears in Weeks (1987) Cell 51: 861-867. The prodomain likely extends from the signal peptide cleavage site to residue 246; the mature protein likely is defined by residues 247-360.

10 "Vgr-1(fx)" refers to protein sequences encoded by the murine Vgr-1 gene and defining the conserved seven cysteine skeleton (Seq. ID No. 13). The amino acid sequence for the full length protein appears in Lyons, et al, (1989) PNAS 86: 4554-4558. The prodomain likely extends from the signal peptide cleavage site to residue 299; the mature protein likely is defined by residues 300-438.

25 "GDF-1(fx)" refers to protein sequences encoded by the human GDF-1 gene and defining the conserved seven cysteine skeleton (Seq. ID No. 14). The cDNA and encoded amino sequence for the full length protein is

provided in Seq. ID. No. 32. The prodomain likely extends from the signal peptide cleavage site to residue 214; the mature protein likely is defined by residues 215-372.

"60A"

refers generically to the morphogenically active proteins expressed from part or all of a DNA sequence (from the Drosophila 60A gene) encoding the 60A proteins (see Seq. ID No. 24 wherein the cDNA and encoded amino acid sequence for the full length protein is provided). "60A(fx)" refers to the protein sequences defining the conserved seven cysteine skeleton (residues 354 to 455 of Seq. ID No. 24.) The prodomain likely extends from the signal peptide cleavage site to residue 324; the mature protein likely is defined by residues 325-455.

"BMP3(fx)"

refers to protein sequences encoded by the human BMP3 gene and defining the conserved seven cysteine skeleton (Seq. ID No. 26). The amino acid sequence for the full length protein appears in Wozney et al. (1988) Science 242: 1528-1534. The prodomain likely extends from the signal peptide cleavage site to residue 290; the mature protein likely is defined by residues 291-472.

- "BMP5(fx)" refers to protein sequences encoded by the human BMP5 gene and defining the conserved seven cysteine skeleton (Seq. ID No. 27). The amino acid sequence for the full length protein appears in Celeste, et al. (1991) PNAS 87: 9843-9847. The pro domain likely extends from the signal peptide cleavage site to residue 316; the mature protein likely is defined by residues 317-454.
- "BMP6(fx)" refers to protein sequences encoded by the human BMP6 gene and defining the conserved seven cysteine skeleton (Seq. ID No. 28). The amino acid sequence for the full length protein appears in Celeste, et al. (1990) PNAS 87: 9843-5847. The pro domain likely includes extends from the signal peptide cleavage site to residue 374; the mature sequence likely includes residues 375-513.

The OP-2 proteins have an additional cysteine residue in this region (e.g., see residue 41 of Seq. ID Nos. 7 and 8), in addition to the conserved cysteine skeleton in common with the other proteins in this family. The GDF-1 protein has a four amino acid insert within the conserved skeleton (residues 44-47 of Seq. ID No. 14) but this insert likely does not interfere with the relationship of the cysteines in the folded structure. In addition, the CBMP2 proteins are missing one amino acid residue within the cysteine skeleton.

The morphogens are inactive when reduced, but are active as oxidized homodimers and when oxidized in combination with other morphogens of this invention (e.g., as heterodimers). Thus, as defined herein, a morphogen is a dimeric protein comprising a pair of polypeptide chains, wherein each polypeptide chain comprises at least the C-terminal six cysteine skeleton defined by residues 43-139 of Seq. ID No. 5, including functionally equivalent arrangements of these cysteines (e.g., amino acid insertions or deletions which alter the linear arrangement of the cysteines in the sequence but not their relationship in the folded structure), such that, when the polypeptide chains are folded, the dimeric protein species comprising the pair of polypeptide chains has the appropriate three-dimensional structure, including the appropriate intra- or inter-chain disulfide bonds such that the protein is capable of acting as a morphogen as defined herein. Specifically, the morphogens generally are capable of all of the following biological functions in a morphogenically permissive environment: stimulating proliferation of progenitor cells; stimulating the differentiation of progenitor cells; stimulating the proliferation of differentiated cells; and supporting the growth and maintenance of differentiated cells, including the "redifferentiation" of transformed cells. In addition, it is also anticipated that these morphogens are capable of inducing redifferentiation of committed cells under appropriate environmental conditions.

In one preferred aspect, the morphogens of this invention comprise one of two species of generic amino acid sequences: Generic Sequence 1 (Seq. ID No. 1) or Generic Sequence 2 (Seq. ID No. 2); where each Xaa

10

Preferred amino acid sequences within the foregoing generic sequences include: Generic Sequence 3 (Seq. ID No. 3), Generic Sequence 4 (Seq. ID No. 4), Generic Sequence 5 (Seq. ID No. 30) and Generic Sequence 6 (Seq. ID No. 31), listed below. These Generic Sequences accommodate the homologies shared among the various preferred members of this morphogen family identified in Table II, as well as the amino acid sequence variation among them. Specifically, Generic Sequences 3 and 4 are composite amino acid sequences of the following proteins presented in Table II and identified in Seq. ID Nos. 5-14: human OP-1 (hOP-1, Seq. ID Nos. 5 and 16-17), mouse OP-1 (mOP-1, Seq. ID Nos. 6 and 18-19), human and mouse OP-2 (Seq. ID Nos. 7, 8, and 20-22), CBMP2A (Seq. ID No. 9), CBMP2B (Seq. ID No. 10), DPP (from Drosophila, Seq. ID No. 11), Vgl, (from Xenopus, Seq. ID No. 12), Vgr-1 (from mouse, Seq. ID No. 13), and GDF-1 (from mouse, Seq. ID No. 14.) The generic sequences include both the amino acid identity shared by the sequences in Table II, as well as alternative residues for the variable positions within the sequence. Note that

- 22 -

these generic sequences allow for an additional cysteine at position 41 or 46 in Generic Sequences 3 or 4, respectively, providing an appropriate cysteine skeleton where inter- or intramolecular disulfide bonds can form, and contain certain critical amino acids which influence the tertiary structure of the proteins.

Generic Sequence 3

Leu Tyr Val Xaa Phe

10	1	5
	Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa	
	10	
	Xaa Ala Pro Xaa Gly Xaa Xaa Ala	
	15	20
15	Xaa Tyr Cys Xaa Gly Xaa Cys Xaa	
	25	30
	Xaa Pro Xaa Xaa Xaa Xaa Xaa	
	35	
	Xaa Xaa Xaa Asn His Ala Xaa Xaa	
20	40	45
	Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa	
	50	
	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys	
	55	60
25	Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa	
	65	

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Xaa Xaa Xaa L u Xaa Xaa Xaa

70

75

Xaa Xaa Xaa Xaa Val Xaa Leu Xaa

80

5 Xaa Xaa Xaa Xaa Met Xaa Val Xaa

85

90

Xaa Cys Gly Cys Xaa

95

wherein each Xaa is independently selected from a group
 10 of one or more specified amino acids defined as
 follows: "Res." means "residue" and Xaa at res.4 =
 (Ser, Asp or Glu); Xaa at res.6 = (Arg, Gln, Ser or
 Lys); Xaa at res.7 = (Asp or Glu); Xaa at res.8 = (Leu
 or Val); Xaa at res.11 = (Gln, Leu, Asp, His or Asn);
 15 Xaa at res.12 = (Asp, Arg or Asn); Xaa at res.14 = (Ile
 or Val); Xaa at res.15 = (Ile or Val); Xaa at res.18 =
 (Glu, Gln, Leu, Lys, Pro or Arg); Xaa at res.20 = (Tyr
 or Phe); Xaa at res.21 = (Ala, Ser, Asp, Met, His, Leu
 or Gln); Xaa at res.23 = (Tyr, Asn or Phe); Xaa at
 20 res.26 = (Glu, His, Tyr, Asp or Gln); Xaa at res.28 =
 (Glu, Lys, Asp or Gln); Xaa at res.30 = (Ala, Ser, Pro
 or Gln); Xaa at res.31 = (Phe, Leu or Tyr); Xaa at
 res.33 = (Leu or Val); Xaa at res.34 = (Asn, Asp, Ala
 or Thr); Xaa at res.35 = (Ser, Asp, Glu, Leu or Ala);
 25 Xaa at res.36 = (Tyr, Cys, His, Ser or Ile); Xaa at
 res.37 = (Met, Phe, Gly or Leu); Xaa at res.38 = (Asn
 or Ser); Xaa at res.39 = (Ala, Ser or Gly); Xaa at
 res.40 = (Thr, Leu or Ser); Xaa at res.44 = (Ile or
 Val); Xaa at res.45 = (Val or Leu); Xaa at res.46 =
 30 (Gln or Arg); Xaa at res.47 = (Thr, Ala or Ser); Xaa at
 res.49 = (Val or Met); Xaa at res.50 = (His or Asn);
 Xaa at res.51 = (Phe, Leu, Asn, Ser, Ala or Val); Xaa

at res.52 = (Ile, Met, Asn, Ala or Val); Xaa at r s.53 = (Asn, Lys, Ala or Glu); Xaa at res.54 = (Pro or Ser); Xaa at res.55 = (Glu, Asp, Asn, or Gly); Xaa at res.56 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser or Ala); Xaa at
5 res.57 = (Val, Ala or Ile); Xaa at res.58 = (Pro or Asp); Xaa at res.59 = (Lys or Leu); Xaa at res.60 = (Pro or Ala); Xaa at res.63 = (Ala or Val); Xaa at res.65 = (Thr or Ala); Xaa at res.66 = (Gln, Lys, Arg or Glu); Xaa at res.67 = (Leu, Met or Val); Xaa at
10 res.68 = (Asn, Ser or Asp); Xaa at res.69 = (Ala, Pro or Ser); Xaa at res.70 = (Ile, Thr or Val); Xaa at res.71 = (Ser or Ala); Xaa at res.72 = (Val or Met); Xaa at res.74 = (Tyr or Phe); Xaa at res.75 = (Phe, Tyr or Leu); Xaa at res.76 = (Asp or Asn); Xaa at res.77 = (Asp, Glu, Asn or Ser); Xaa at res.78 = (Ser, Gln, Asn or Tyr); Xaa at res.79 = (Ser, Asn, Asp or Glu); Xaa at
15 res.80 = (Asn, Thr or Lys); Xaa at res.82 = (Ile or Val); Xaa at res.84 = (Lys or Arg); Xaa at res.85 = (Lys, Asn, Gln or His); Xaa at res.86 = (Tyr or His); Xaa at res.87 = (Arg, Gln or Glu); Xaa at res.88 = (Asn, Glu or Asp); Xaa at res.90 = (Val, Thr or Ala); Xaa at res.92 = (Arg, Lys, Val, Asp or Glu); Xaa at
20 res.93 = (Ala, Gly or Glu); and Xaa at res.97 = (His or Arg);

25

Generic Sequence 4

	Cys	Xaa	Xaa	Xaa	Xaa	Leu	Tyr	Val	Xaa	Phe
	1				5					10
30	Xaa	Xaa	Xaa	Gly	Trp	Xaa	Xaa	Trp	Xaa	
				15						
	Xaa	Ala	Pro	Xaa	Gly	Xaa	Xaa	Ala		
	20					25				
	Xaa	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa		
35			30					35		

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Xaa Pro Xaa Xaa Xaa Xaa Xaa
 40
 Xaa Xaa Xaa Asn His Ala Xaa Xaa
 45 50
 5 Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa
 55
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 60 65
 Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
 10 70
 Xaa Xaa Xaa Leu Xaa Xaa Xaa
 75 80
 Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
 85
 15 Xaa Xaa Xaa Xaa Met Xaa Val Xaa
 90 95
 Xaa Cys Gly Cys Xaa
 100

wherein each Xaa is independently selected from a group
 20 of one or more specified amino acids as defined by the
 following: "Res." means "residue" and Xaa at res.2 =
 (Lys or Arg); Xaa at res.3 = (Lys or Arg); Xaa at res.4
 = (His or Arg); Xaa at res.5 = (Glu, Ser, His, Gly, Arg
 or Pro); Xaa at res.9 = (Ser, Asp or Glu); Xaa at
 25 res.11 = (Arg, Gln, Ser or Lys); Xaa at res.12 = (Asp
 or Glu); Xaa at res.13 = (Leu or Val); Xaa at res.16 =
 (Gln, Leu, Asp, His or Asn); Xaa at res.17 = (Asp, Arg,
 or Asn); Xaa at res.19 = (Ile or Val); Xaa at res.20 =
 (Ile or Val); Xaa at res.23 = (Glu, Gln, Leu, Lys, Pro
 30 or Arg); Xaa at res.25 = (Tyr or Phe); Xaa at res.26 =
 (Ala, Ser, Asp, Met, His, Leu, or Gln); Xaa at res.28 =
 (Tyr, Asn or Phe); Xaa at res.31 = (Glu, His, Tyr, Asp
 or Gln); Xaa at res.33 = Glu, Lys, Asp or Gln); Xaa at
 res.35 = (Ala, Ser or Pro); Xaa at res.36 = (Phe, Leu
 35 or Tyr); Xaa at res.38 = (Leu or Val); Xaa at res.39 =

(Asn, Asp, Ala or Thr); Xaa at res.40 = (Ser, Asp, Glu, Leu or Ala); Xaa at res.41 = (Tyr, Cys, His, Ser or Ile); Xaa at res.42 = (Met, Phe, Gly or Leu); Xaa at res.44 = (Ala, Ser or Gly); Xaa at res.45 = (Thr, Leu or Ser); Xaa at res.49 = (Ile or Val); Xaa at res.50 = (Val or Leu); Xaa at res.51 = (Gln or Arg); Xaa at res.52 = (Thr, Ala or Ser); Xaa at res.54 = (Val or Met); Xaa at res.55 = (His or Asn); Xaa at res.56 = (Phe, Leu, Asn, Ser, Ala or Val); Xaa at res.57 = (Ile, Met, Asn, Ala or Val); Xaa at res.58 = (Asn, Lys, Ala or Glu); Xaa at res.59 = (Pro or Ser); Xaa at res.60 = (Glu, Asp, or Gly); Xaa at res.61 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser or Ala); Xaa at res.62 = (Val, Ala or Ile); Xaa at res.63 = (Pro or Asp); Xaa at res.64 = (Lys or Leu); Xaa at res.65 = (Pro or Ala); Xaa at res.68 = (Ala or Val); Xaa at res.70 = (Thr or Ala); Xaa at res.71 = (Gln, Lys, Arg or Glu); Xaa at res.72 = (Leu, Met or Val); Xaa at res.73 = (Asn, Ser or Asp); Xaa at res.74 = (Ala, Pro or Ser); Xaa at res.75 = (Ile, Thr or Val); Xaa at res.76 = (Ser or Ala); Xaa at res.77 = (Val or Met); Xaa at res.79 = (Tyr or Phe); Xaa at res.80 = (Phe, Tyr or Leu); Xaa at res.81 = (Asp or Asn); Xaa at res.82 = (Asp, Glu, Asn or Ser); Xaa at res.83 = (Ser, Gln, Asn or Tyr); Xaa at res.84 = (Ser, Asn, Asp or Glu); Xaa at res.85 = (Asn, Thr or Lys); Xaa at res.87 = (Ile or Val); Xaa at res.89 = (Lys or Arg); Xaa at res.90 = (Lys, Asn, Gln or His); Xaa at res.91 = (Tyr or His); Xaa at res.92 = (Arg, Gln or Glu); Xaa at res.93 = (Asn, Glu or Asp); Xaa at res.95 = (Val, Thr or Ala); Xaa at res.97 = (Arg, Lys, Val, Asp or Glu); Xaa at res.98 = (Ala, Gly or Glu); and Xaa at res.102 = (His or Arg).

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Similarly, Generic Sequence 5 (Seq. ID No. 30) and Generic Sequence 6 (Seq. ID No. 31) accommodate the homologies shared among all the morphogen protein family members identified in Table II. Specifically, Generic Sequences 5 and 6 are composite amino acid sequences of human OP-1 (hOP-1, Seq. ID Nos. 5 and 16-17), mouse OP-1 (mOP-1, Seq. ID Nos. 6 and 18-19), human and mouse OP-2 (Seq. ID Nos. 7, 8, and 20-22), CBMP2A (Seq. ID No. 9), CBMP2B (Seq. ID No. 10), DPP (from Drosophila, Seq. ID No. 11), Vgl, (from Xenopus, Seq. ID No. 12), Vgr-1 (from mouse, Seq. ID No. 13), and GDF-1 (from mouse, Seq. ID No. 14), human BMP3 (Seq. ID No. 26), human BMP5 (Seq. ID No. 27), human BMP6 (Seq. ID No. 28) and 60(A) (from Drosophila, Seq. ID Nos. 24-25). The generic sequences include both the amino acid identity shared by these sequences in the C-terminal domain, defined by the six and seven cysteine skeletons (Generic Sequences 5 and 6, respectively), as well as alternative residues for the variable positions within the sequence. As for Generic Sequences 3 and 4, Generic Sequences 5 and 6 allow for an additional cysteine at position 41 (Generic Sequence 5) or position 46 (Generic Sequence 6), providing an appropriate cysteine skeleton where inter- or intramolecular disulfide bonds can form, and containing certain critical amino acids which influence the tertiary structure of the proteins.

Generic Sequence 5

30

Leu Xaa Xaa Xaa Phe

1

5

Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa

10

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	Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Ala
	15						20	
	Xaa	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa
		25						30
5	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	
					35			
	Xaa	Xaa	Xaa	Asn	His	Ala	Xaa	Xaa
		40						45
	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
10					50			
	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys
		55						60
	Cys	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa
					65			
15	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	
		70					75	
	Xaa	Xaa	Xaa	Xaa	Val	Xaa	Leu	Xaa
					80			
	Xaa	Xaa	Xaa	Xaa	Met	Xaa	Val	Xaa
20		85					90	
	Xaa	Cys	Xaa	Cys	Xaa			
					95			

wherein each Xaa is independently selected from a group of one or more specified amino acids defined as follows: "Res." means "residue" and Xaa at res.2 = (Tyr or Lys); Xaa at res.3 = Val or Ile); Xaa at res.4 = (Ser, Asp or Glu); Xaa at res.6 = (Arg, Gln, Ser, Lys or Ala); Xaa at res.7 = (Asp, Glu or Lys); Xaa at res.8

= (Leu, Val or Ile); Xaa at res.11 = (Gln, Leu, Asp, His, Asn or Ser); Xaa at res.12 = (Asp, Arg, Asn or Glu); Xaa at res.14 = (Ile or Val); Xaa at res.15 = (Ile or Val); Xaa at res.16 (Ala or Ser); Xaa at res.18
5 = (Glu, Gln, Leu, Lys, Pro or Arg); Xaa at res.19 = (Gly or Ser); Xaa at res.20 = (Tyr or Phe); Xaa at res.21 = (Ala, Ser, Asp, Met, His, Gln, Leu or Gly); Xaa at res.23 = (Tyr, Asn or Phe); Xaa at res.26 = (Glu, His, Tyr, Asp, Gln or Ser); Xaa at res.28 = (Glu,
10 Lys, Asp, Gln or Ala); Xaa at res.30 = (Ala, Ser, Pro, Gln or Asn); Xaa at res.31 = (Phe, Leu or Tyr); Xaa at res.33 = (Leu, Val or Met); Xaa at res.34 = (Asn, Asp, Ala, Thr or Pro); Xaa at res.35 = (Ser, Asp, Glu, Leu, Ala or Lys); Xaa at res.36 = (Tyr, Cys, His, Ser or
15 Ile); Xaa at res.37 = (Met, Phe, Gly or Leu); Xaa at res.38 = (Asn, Ser or Lys); Xaa at res.39 = (Ala, Ser, Gly or Pro); Xaa at res.40 = (Thr, Leu or Ser); Xaa at res.44 = (Ile, Val or Thr); Xaa at res.45 = (Val, Leu or Ile); Xaa at res.46 = (Gln or Arg); Xaa at res.47 =
20 (Thr, Ala or Ser); Xaa at res.48 = (Leu or Ile); Xaa at res.49 = (Val or Met); Xaa at res.50 = (His, Asn or Arg); Xaa at res.51 = (Phe, Leu, Asn, Ser, Ala or Val); Xaa at res.52 = (Ile, Met, Asn, Ala, Val or Leu); Xaa at res.53 = (Asn, Lys, Ala, Glu, Gly or Phe); Xaa at
25 res.54 = (Pro, Ser or Val); Xaa at res.55 = (Glu, Asp, Asn, Gly, Val or Lys); Xaa at res.56 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser, Ala, Pro or His); Xaa at res.57 = (Val, Ala or Ile); Xaa at res.58 = (Pro or Asp); Xaa at res.59 = (Lys, Leu or Glu); Xaa at res.60 = (Pro or
30 Ala); Xaa at res.63 = (Ala or Val); Xaa at res.65 = (Thr, Ala or Glu); Xaa at res.66 = (Gln, Lys, Arg or Glu); Xaa at res.67 = (Leu, Met or Val); Xaa at res.68 = (Asn, Ser, Asp or Gly); Xaa at res.69 = (Ala, Pro or Ser); Xaa at res.70 = (Ile, Thr, Val or Leu); Xaa at
35 res.71 = (Ser, Ala or Pro); Xaa at res.72 = (Val, Met

- 30 -

or Ile); Xaa at res.74 = (Tyr or Phe); Xaa at res.75 =
 (Phe, Tyr, Leu or His); Xaa at res.76 = (Asp, Asn or
 Leu); Xaa at res.77 = (Asp, Glu, Asn or Ser); Xaa at
 res.78 = (Ser, Gln, Asn, Tyr or Asp); Xaa at res.79 =
 5 (Ser, Asn, Asp, Glu or Lys); Xaa at res.80 = (Asn, Thr
 or Lys); Xaa at res.82 = (Ile, Val or Asn); Xaa at
 res.84 = (Lys or Arg); Xaa at res.85 = (Lys, Asn, Gln,
 His or Val); Xaa at res.86 = (Tyr or His); Xaa at
 res.87 = (Arg, Gln, Glu or Pro); Xaa at res.88 = (Asn,
 10 Glu or Asp); Xaa at res.90 = (Val, Thr, Ala or Ile);
 Xaa at res.92 = (Arg, Lys, Val, Asp or Glu); Xaa at
 res.93 = (Ala, Gly, Glu or Ser); Xaa at res.95 = (Gly
 or Ala) and Xaa at res.97 = (His or Arg).

15

Generic Sequence 6

Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe
 1 5 10
 Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
 15
 20 Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala
 20 25
 Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
 30 35
 25 Xaa Pro Xaa Xaa Xaa Xaa Xaa
 40
 Xaa Xaa Xaa Asn His Ala Xaa Xaa
 45 50
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 55
 30 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 60 65
 Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
 70

- 31 -

Xaa Xaa Xaa Leu Xaa Xaa Xaa
 75 80
 Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
 85
 5 Xaa Xaa Xaa Xaa Met Xaa Val Xaa
 90 95
 Xaa Cys Xaa Cys Xaa
 100

- 10 wherein each Xaa is independently selected from a group
 of one or more specified amino acids as defined by the
 following: "Res." means "residue" and Xaa at res.2 =
 (Lys, Arg, Ala or Gln); Xaa at res.3 = (Lys, Arg or
 Met); Xaa at res.4 = (His, Arg or Gln); Xaa at res.5 =
 15 (Glu, Ser, His, Gly, Arg, Pro, Thr, or Tyr); Xaa at
 res.7 = (Tyr or Lys); Xaa at res.8 = (Val or Ile); Xaa
 at res.9 = (Ser, Asp or Glu); Xaa at res.11 = (Arg,
 Gln, Ser, Lys or Ala); Xaa at res.12 = (Asp, Glu, or
 Lys); Xaa at res.13 = (Leu, Val or Ile); Xaa at res.16
 20 = (Gln, Leu, Asp, His, Asn or Ser); Xaa at res.17 =
 (Asp, Arg, Asn or Glu); Xaa at res.19 = (Ile or Val);
 Xaa at res.20 = (Ile or Val); Xaa at res.21 = (Ala or
 Ser); Xaa at res.23 = (Glu, Gln, Leu, Lys, Pro or Arg);
 Xaa at res.24 = (Gly or Ser); Xaa at res.25 = (Tyr or
 25 Phe); Xaa at res.26 = (Ala, Ser, Asp, Met, His, Gln,
 Leu, or Gly); Xaa at res.28 = (Tyr, Asn or Phe); Xaa at
 res.31 = (Glu, His, Tyr, Asp, Gln or Ser); Xaa at
 res.33 = Glu, Lys, Asp, Gln or Ala); Xaa at res.35 =
 (Ala, Ser, Pro, Gln or Asn); Xaa at res.36 = (Phe, Leu
 30 or Tyr); Xaa at res.38 = (Leu, Val or Met); Xaa at
 res.39 = (Asn, Asp, Ala, Thr or Pro); Xaa at res.40 =
 (Ser, Asp, Glu, Leu, Ala or Lys); Xaa at res.41 = (Tyr,
 Cys, His, Ser or Ile); Xaa at res.42 = (Met, Phe, Gly
 or Leu); Xaa at res.43 = (Asn, Ser or Lys); Xaa at
 35 res.44 = (Ala, Ser, Gly or Pro); Xaa at res.45 = (Thr,

Leu or Ser); Xaa at res.49 = (Ile, Val or Thr); Xaa at
res.50 = (Val, Leu or Ile); Xaa at res.51 = (Gln or
Arg); Xaa at res.52 = (Thr, Ala or Ser); Xaa at res.53
= (Leu or Ile); Xaa at res.54 = (Val or Met); Xaa at
5 res.55 = (His, Asn or Arg); Xaa at res.56 = (Phe, Leu,
Asn, Ser, Ala or Val); Xaa at res.57 = (Ile, Met, Asn,
Ala, Val or Leu); Xaa at res.58 = (Asn, Lys, Ala, Glu,
Gly or Phe); Xaa at res.59 = (Pro, Ser or Val); Xaa at
res.60 = (Glu, Asp, Gly, Val or Lys); Xaa at res.61 =
10 (Thr, Ala, Val, Lys, Asp, Tyr, Ser, Ala, Pro or His);
Xaa at res.62 = (Val, Ala or Ile); Xaa at res.63 = (Pro
or Asp); Xaa at res.64 = (Lys, Leu or Glu); Xaa at
res.65 = (Pro or Ala); Xaa at res.68 = (Ala or Val);
Xaa at res.70 = (Thr, Ala or Glu); Xaa at res.71 =
15 (Gln, Lys, Arg or Glu); Xaa at res.72 = (Leu, Met or
Val); Xaa at res.73 = (Asn, Ser, Asp or Gly); Xaa at
res.74 = (Ala, Pro or Ser); Xaa at res.75 = (Ile, Thr,
Val or Leu); Xaa at res.76 = (Ser, Ala or Pro); Xaa at
res.77 = (Val, Met or Ile); Xaa at res.79 = (Tyr or
20 Phe); Xaa at res.80 = (Phe, Tyr, Leu or His); Xaa at
res.81 = (Asp, Asn or Leu); Xaa at res.82 = (Asp, Glu,
Asn or Ser); Xaa at res.83 = (Ser, Gln, Asn, Tyr or
Asp); Xaa at res.84 = (Ser, Asn, Asp, Glu or Lys); Xaa
at res.85 = (Asn, Thr or Lys); Xaa at res.87 = (Ile,
25 Val or Asn); Xaa at res.89 = (Lys or Arg); Xaa at
res.90 = (Lys, Asn, Gln, His or Val); Xaa at res.91 =
(Tyr or His); Xaa at res.92 = (Arg, Gln, Glu or Pro);
Xaa at res.93 = (Asn, Glu or Asp); Xaa at res.95 =
(Val, Thr, Ala or Ile); Xaa at res.97 = (Arg, Lys, Val,
30 Asp or Glu); Xaa at res.98 = (Ala, Gly, Glu or Ser);
Xaa at res.100 = (Gly or Ala); and Xaa at res.102 =
(His or Arg).

Particularly useful sequences for use as morphogens in this invention include the C-terminal domains, e.g., the C-terminal 96-102 amino acid residues of Vgl, Vgr-1, DPP, OP-1, OP-2, CBMP-2A, CBMP-2B, GDF-1 (see Table II, below, and Seq. ID Nos. 5-14), as well as proteins comprising the C-terminal domains of 60A, BMP3, BMP5 and BMP6 (see Seq. ID Nos. 24-28), all of which include at least the conserved six or seven cysteine skeleton. In addition, biosynthetic constructs designed from the generic sequences, such as COP-1, 3-5, 7, 16, disclosed in U.S. Pat. No. 5,011,691, also are useful. Other sequences include the inhibins/activin proteins (see, for example, U.S. Pat. Nos. 4,968,590 and 5,011,691). Accordingly, other useful sequences are those sharing at least 70% amino acid sequence homology or "similarity", and preferably 80% homology or similarity with any of the sequences above. These are anticipated to include allelic and species variants and mutants, and biosynthetic muteins, as well as novel members of this morphogenic family of proteins. Particularly envisioned in the family of related proteins are those proteins exhibiting morphogenic activity and wherein the amino acid changes from the preferred sequences include conservative changes, e.g., those as defined by Dayoff et al., Atlas of Protein Sequence and Structure; vol. 5, Suppl. 3, pp. 345-362, (M.O. Dayoff, ed., Nat'l BioMed. Research Fdn., Washington, D.C. 1979). As used herein, potentially useful sequences are aligned with a known morphogen sequence using the method of Needleman et al. ((1970) J.Mol.Biol. 48:443-453) and identities calculated by the Align program (DNASTar, Inc.). "Homology" or "similarity" as used herein includes allowed conservative changes as defined by Dayoff et al.

Th currently most preferred protein sequences useful as morphogens in this invention include those having greater than 60% identity, preferably greater than 65% identity, with the amino acid sequence defining the conserved six cysteine skeleton of hOP1 (e.g., residues 43-139 of Seq. ID No. 5). These most preferred sequences include both allelic and species variants of the OP-1 and OP-2 proteins, including the *Drosophila* 60A protein. Accordingly, in another preferred aspect of the invention, useful morphogens include active proteins comprising species of polypeptide chains having the generic amino acid sequence herein referred to as "OPX", which accommodates the homologies between the various identified species of OP1 and OP2 (Seq. ID No. 29).

The morphogens useful in the methods, composition and devices of this invention include proteins comprising any of the polypeptide chains described above, whether isolated from naturally-occurring sources, or produced by recombinant DNA or other synthetic techniques, and includes allelic and species variants of these proteins, naturally-occurring or biosynthetic mutants thereof, as well as various truncated and fusion constructs. Deletion or addition mutants also are envisioned to be active, including those which may alter the conserved C-terminal cysteine skeleton, provided that the alteration does not functionally disrupt the relationship of these cysteines in the folded structure. Accordingly, such active forms are considered the equivalent of the specifically described constructs disclosed herein.

The proteins may include forms having varying glycosylation patterns, varying N-termini, a family of related proteins having regions of amino acid sequence homology, and active truncated or mutated forms of
5 native or biosynthetic proteins, produced by expression of recombinant DNA in host cells.

The morphogenic proteins can be expressed from intact or truncated cDNA or from synthetic DNAs in
10 procaryotic or eucaryotic host cells, and purified, cleaved, refolded, and dimerized to form morphogenically active compositions. Currently preferred host cells include E. coli or mammalian cells, such as CHO, COS or BSC cells. A detailed
15 description of the morphogens useful in the methods, compositions and devices of this invention is disclosed in copending US patent application Serial Nos. 752,764, filed August 30, 1991, and 667,274, filed March 11, 1991, the disclosure of which are incorporated herein
20 by reference.

Thus, in view of this disclosure, skilled genetic engineers can isolate genes from cDNA or genomic libraries of various different species which encode
25 appropriate amino acid sequences, or construct DNAs from oligonucleotides, and then can express them in various types of host cells, including both procaryotes and eucaryotes, to produce large quantities of active proteins capable of protecting tissues and organs from
30 immune cell-mediated tissue destruction, including substantially inhibiting such damage and/or regenerating the damaged tissue in a variety of mammals, including humans.

The foregoing and other objects, features and advantages of the present invention will be made more apparent from the following detailed description of the invention.

Brief Description of the Drawings

- FIG 1 shows the cardioprotective effects of morphogen (hOP1) in a rat myocardial ischemia-reperfusion model, as evidenced by the smaller loss of myocardial creatine kinase in hOP1-treated rats;
- FIG 2 shows the effects of 20 μ g of morphogen (hOP1) given 24 hours prior to isolation of rat heart on endothelial-dependent vasorelaxation to acetylcholine following induced ischemia-reperfusion injury;
- FIG 3 shows the effect of morphogen (hOP1) on neutrophil adherence to LTB₄-stimulated mesenteric artery endothelium in neutrophil-activated rats;
- FIG 4 (A and B) are schematic representations of morphogen inhibition of early mononuclear phagocytic multinuclearization in vivo;
- FIG 5 graphs the effect of a morphogen (e.g., OP-1) and a placebo control on mucositis lesion formation; and
- FIG 6 (A-D) graphs the effects of a morphogen (eg., OP-1, Figs. 6A and 6C) and TGF- β (Fig. 6B and 6D) on collagen (6A and 6B) and hyaluronic acid (6C and 6D) production in primary fibroblast cultures.

Detailed Description of the Invention

It now has been surprisingly discovered that the morphogens defined herein are effective agents in alleviating the tissue destructive effects associated with the body's inflammatory response to tissue injury. In particular, as disclosed herein, the morphogens are capable of alleviating the necrotic tissue effects associated with the ensuing inflammatory responses that occur following an initial tissue injury.

When tissue injury occurs, whether caused by bacteria, trauma, chemicals, heat, or any other phenomenon, the body's inflammatory response is stimulated. In response to signals released from the damaged cells (e.g., cytokines), extravascularization of immune effector cells is induced. Under ordinary circumstances these invading immune effector cells kill the infectious agent and/or infected or damaged cells (through the release of killing substances such as superoxides, perforins, and other antimicrobial agents stored in granules), remove the dead tissues and organisms (through phagocytosis), release various biological response modifiers that promote rapid healing and covering of the wound (quite often resulting in the formation of fibrotic scar tissue), and then, after the area is successfully healed, exit from the site of the initial insult. Once the site is perceived to be normal, the local release of inflammatory cytokines ceases and the display of adhesion molecules on the vessel endothelium returns to basal levels. In some cases, however, the zeal of these interacting signals and cellular systems, which are designed to capture and contain very rapidly multiplying infectious agents, act to the detriment of

the body, killing additional, otherwise healthy, surrounding tissue. This additional unnecessary tissue death further compromises organ function and sometimes results in death of the individual. In addition, the resulting scar tissue that often forms can interfere with normal tissue function as occurs, for example, in idiopathic pulmonary fibrosis, IBD and organ cirrhosis.

The vascular endothelium constitutes the first barrier between circulating immune effector cells and extravascular tissues. Extravasation of these circulating cells requires that they bind to the vascular endothelial cells, cross the basement membrane, and enter insulted tissues e.g., by phagocytosis or protease-mediated extracellular matrix degradation. Without being limited to a particular theory, it is believed that the morphogens of this invention may modulate the inflammatory response in part by modulating the attachment of immune effector cells to the luminal side of the endothelium of blood vessels at or near sites of tissue damage and/or inflammatory lesions. Because the method reduces or prevents the attachment of immune effector cells at these sites, it also prevents the subsequent release of tissue destructive agents by these same immune effector cells at sites of tissue damage and/or inflammatory lesions. Because attachment of immune effector cells to the endothelium must precede their extravascularization, the method also prevents the initial or continued entry of these cells into extravascular sites of tissue destruction or ongoing inflammatory lesions. Therefore, the invention not only relates to a method to reduce or prevent the immune cell-mediated cellular destruction at extravascular sites of recent tissue destruction, but

also relates to a method to prevent or reduce the continued entry of immune effector cells into extravascular sites of ongoing inflammatory cascades. As will be appreciated by those skilled in the art, the morphogens of this invention also may be contemplated in mechanisms for disrupting the functional interaction of immune effector cells with endothelium where the adhesion molecules are induced by means other than in response to tissue injury.

10

One source of tissue injury is induced by cell exposure to toxic oxygen concentrations, such as ischemic-reperfusion tissue injury (oxygen deprivation), and following hyperoxia injury (lethally high oxygen concentrations). Accordingly, the process of the present invention provides a method for alleviating the tissue damage induced by ischemic-reperfusion injury or hyperoxia-induced injury comprising the step of administering to the afflicted individual a therapeutic amount of a morphogen prior to, during, or after damage to the affected tissue. Where the toxic oxygen concentrations may be deliberately induced, as by a surgical or clinical procedure, the morphogen preferably is administered prior to induction.

25

In addition, the morphogens described herein, in contrast to fibrogenic growth factors such as TGF- β , stimulate tissue morphogenesis and do not stimulate fibrosis or scar tissue formation (see Example 9, below.) Accordingly, in addition to inhibiting the tissue destructive effects associated with the inflammatory response, the morphogens further enhance the viability of damaged tissue and/or organs by stimulating the regeneration of the damaged tissue and preventing fibrogenesis.

35

Th morphogens described herein also can inhibit epithelial cell proliferation (see Example 10, below.) This activity of the morphogens also may be particularly useful in the treatment of psoriasis and other inflammatory diseases that involve epithelial cell populations.

Provided below are detailed descriptions of suitable morphogens useful in the methods and compositions of this invention, as well as methods for their administration and application, and numerous, nonlimiting examples which 1) illustrate the suitability of the morphogens and morphogen-stimulating agents described herein as therapeutic agents for protecting tissue from the tissue destructive effects associated with the body's inflammatory response; and 2) provide assays with which to test candidate morphogens and morphogen-stimulating agents for their efficacy.

20

I. Useful Morphogens

As defined herein a protein is morphogenic if it is capable of inducing the developmental cascade of cellular and molecular events that culminate in the formation of new, organ-specific tissue and comprises at least the conserved C-terminal six cysteine skeleton or its functional equivalent (see supra).

Specifically, the morphogens generally are capable of all of the following biological functions in a morphogenically permissive environment: stimulating proliferation of progenitor cells; stimulating the differentiation of progenitor cells; stimulating the proliferation of differentiated cells; and supporting

35

the growth and maintenance of differentiated cells, including the "redifferentiation" of transformed cells. Details of how the morphogens useful in the method of this invention first were identified, as well as a description on how to make, use and test them for morphogenic activity are disclosed in USSN 667,274, filed March 11, 1991 and USSN 752,764, filed August 30, 1991, the disclosures of which are hereinabove incorporated by reference. As disclosed therein, the morphogens may be purified from naturally-sourced material or recombinantly produced from procaryotic or eucaryotic host cells, using the genetic sequences disclosed therein. Alternatively, novel morphogenic sequences may be identified following the procedures disclosed therein.

Particularly useful proteins include those which comprise the naturally derived sequences disclosed in Table II. Other useful sequences include biosynthetic constructs such as those disclosed in U.S. Pat. 5,011,691, the disclosure of which is incorporated herein by reference (e.g., COP-1, COP-3, COP-4, COP-5, COP-7, and COP-16).

Accordingly, the morphogens useful in the methods and compositions of this invention also may be described by morphogenically active proteins having amino acid sequences sharing 70% or, preferably, 80% homology (similarity) with any of the sequences described above, where "homology" is as defined herein above.

Th morphog ns useful in the method of this invention also can be described by any of the 6 generic sequences described herein (Generic Sequences 1, 2, 3, 4, 5 and 6). Generic sequences 1 and 2 also may
 5 include, at their N-terminus, the sequence

Cys Xaa Xaa Xaa Xaa (Seq. ID No. 15)

1

5

10 Table II, set forth below, compares the amino acid sequences of the active regions of native proteins that have been identified as morphogens, including human OP-1 (hOP-1, Seq. ID Nos. 5 and 16-17), mouse OP-1 (mOP-1, Seq. ID Nos. 6 and 18-19), human and mouse OP-2
 15 (Seq. ID Nos. 7, 8, and 20-23), CBMP2A (Seq. ID No. 9), CBMP2B (Seq. ID No. 10), BMP3 (Seq. ID No. 26), DPP (from Drosophila, Seq. ID No. 11), Vgl, (from Xenopus, Seq. ID No. 12), Vgr-1 (from mouse, Seq. ID No. 13), GDF-1 (from mouse, Seq. ID Nos. 14, 32 and 33), 60A
 20 protein (from Drosophila, Seq. ID Nos. 24 and 25), BMP5 (Seq. ID No. 27) and BMP6 (Seq. ID No. 28). The sequences are aligned essentially following the method of Needleman et al. (1970) J. Mol. Biol., 48:443-453, calculated using the Align Program (DNASTar, Inc.) In
 25 the table, three dots indicates that the amino acid in that position is the same as the amino acid in hOP-1. Three dashes indicates that no amino acid is present in that position, and are included for purposes of illustrating homologies. For example, amino acid
 30 residue 60 of CBMP-2A and CBMP-2B is "missing". Of course, both these amino acid sequences in this region comprise Asn-Ser (residues 58, 59), with CBMP-2A then comprising Lys and Ile, whereas CBMP-2B comprises Ser and Ile.

35

TABLE II

	hOP-1	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	
	mOP-1	
5	hOP-2	...	Arg	Arg	
	mOP-2	...	Arg	Arg	
	DPP	...	Arg	Arg	...	Ser	
	Vgl	Lys	Arg	His	
	Vgr-1	Gly	
10	CBMP-2A	Arg	...	Pro	
	CBMP-2B	...	Arg	Arg	...	Ser	
	BMP3	...	Ala	Arg	Arg	Tyr	...	Lys	...	
	GDF-1	...	Arg	Ala	Arg	Arg	
	60A	...	Gln	Met	Glu	Thr	
15	BMP5	
	BMP6	...	Arg	
		1				5				
20	hOP-1	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp
	mOP-1
	hOP-2	Gln	Leu	...
	mOP-2	Ser	Leu	...
	DPP	Asp	...	Ser	...	Val	Asp	...
25	Vgl	Glu	...	Lys	...	Val	Asn
	Vgr-1	Gln	...	Val
	CBMP-2A	Asp	...	Ser	...	Val	Asn	...
	CBMP-2B	Asp	...	Ser	...	Val	Asn	...
	BMP3	Asp	...	Ala	...	Ile	Ser	Glu
30	GDF-1	Glu	Val	His	Arg
	60A	Asp	...	Lys	His	...
	BMP5
	BMP6	Gln
			10					15		

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	hOP-2	Asp	...	Cys
	mOP-2	Asp	...	Cys
	DPP	Ala	Asp	His	Phe	...	Ser
	Vgl	Tyr	Thr	Glu	Ile	Leu	...	Gly
5	Vgr-1	Ala	His
	CBMP-2A	Ala	Asp	His	Leu	...	Ser
	CBMP-2B	Ala	Asp	His	Leu	...	Ser
	GDF-1	Leu	...	Val	Ala	Leu	Ser	Gly	Ser**	...
	BMP3	Met	Pro	Lys	Ser	Leu	Lys	Pro
10	60A	Ala	His
	BMP5	Ala	His	Met
	BMP6	Ala	His	Met
						40				
15	hOP-1	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu
	mOP-1
	hOP-2	Leu	...	Ser	...
	mOP-2	Leu	...	Ser	...
	DPP	Val
20	Vgl	Ser	Leu
	Vgr-1
	CBMP-2A
	CBMP-2B
	BMP3	Ser	Thr	Ile	...	Ser	Ile
25	GDF-1	Leu	Val	Leu	Arg	Ala	...
	60A
	BMP5
	BMP6
		45					50			
30										
	hOP-1	Val	His	Phe	Ile	Asn	Pro	Glu	Thr	Val
	mOP-1	Asp
	hOP-2	...	His	Leu	Met	Lys	...	Asn	Ala	...
35	mOP-2	...	His	Leu	Met	Lys	...	Asp	Val	...

[illegible]

	DPP	...	Asp	Ser	Val	Ala	Met	Leu
	CBMP-2A	...	Ser	Met	Leu
	CBMP-2B	...	Ser	Met	Leu
	BMP3	Met	Ser	Ser	Leu	...	Ile	...	Phe	Tyr
5	GDF-1	...	Ser	Pro	Phe	...
	60A	...	Gly	...	Leu	Pro	His
	BMP5
	BMP6
					75					80
10	hOP-1	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys
	mOP-1
	hOP-2	...	Ser	...	Asn	Arg
	mOP-2	...	Ser	...	Asn	Arg
15	DPP	Asn	...	Gln	...	Thr	...	Val
	Vgl	...	Asn	Asn	Asp	Val	...	Arg
	Vgr-1	Asn
	CBMP-2A	...	Glu	Asn	Glu	Lys	...	Val
	CBMP-2B	...	Glu	Tyr	Asp	Lys	...	Val
20	BMP3	...	Glu	Asn	Lys	Val
	GDF-1	...	Asn	...	Asp	Val	...	Arg
	60A	Leu	Asn	Asp	Glu	Asn
	BMP5
	BMP6	Asn
25						85				
	hOP-1	Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	
	mOP-1	
30	hOP-2	...	His	Lys	
	mOP-2	...	His	Lys	
	DPP	Asn	...	Gln	Glu	...	Thr	...	Val	
	Vgl	His	...	Glu	Ala	...	Asp	
	Vgr-1	
35	CBMP-2A	Asn	...	Gln	Asp	Glu	

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	CBMP-2B	Asn	...	Gln	Glu	Glu
	BMP3	Val	...	Pro	Thr	...	Glu
	GDF-1	Gln	...	Glu	Asp	Asp
	60A	Ile	...	Lys
5	BMP5
	BMP6	Trp
		90					95		
10	hOP-1	Ala	Cys	Gly	Cys	His			
	mOP-1			
	hOP-2			
	mOP-2			
	DPP	Gly	Arg			
15	Vgl	Glu	Arg			
	Vgr-1			
	CBMP-2A	Gly	Arg			
	CBMP-2B	Gly	Arg			
	BMP3	Ser	...	Ala	...	Arg			
20	GDF-1	Glu	Arg			
	60A	Ser			
	BMP5	Ser			
	BMP6			

100

25 **Between residues 56 and 57 of BMP3 is a Val residue;
 between residues 43 and 44 of GDF-1 lies
 the amino acid sequence Gly-Gly-Pro-Pro.

30 As is apparent from the foregoing amino acid
 sequence comparisons, significant amino acid changes
 can be made within the generic sequences while
 retaining the morphogenic activity. For example, while
 the GDF-1 protein sequence depicted in Table II shares
 35 only about 50% amino acid identity with the hOP1

- 50 -

sequence described herein, the GDF-1 sequence shares greater than 70% amino acid sequence homology (or "similarity") with the hOP1 sequence, where "homology" or "similarity" includes allowed conservative amino acid changes within the sequence as defined by Dayoff, et al., Atlas of Protein Sequence and Structure vol.5, supp.3, pp.345-362, (M.O. Dayoff, ed., Nat'l BioMed. Res. Fd'n, Washington D.C. 1979.)

10 The currently most preferred protein sequences useful as morphogens in this invention include those having greater than 60% identity, preferably greater than 65% identity, with the amino acid sequence defining the conserved six cysteine skeleton of hOP1
15 (e.g., residues 43-139 of Seq. ID No. 5). These most preferred sequences include both allelic and species variants of the OP-1 and OP-2 proteins, including the Drosophila 60A protein. Accordingly, in still another preferred aspect, the invention includes morphogens
20 comprising species of polypeptide chains having the generic amino acid sequence referred to herein as "OPX", which defines the seven cysteine skeleton and accommodates the identities between the various identified mouse and human OP1 and OP2 proteins. OPX
25 is presented in Seq. ID No. 29. As described therein, each Xaa at a given position independently is selected from the residues occurring at the corresponding position in the C-terminal sequence of mouse or human OP1 or OP2 (see Seq. ID Nos. 5-8 and/or Seq. ID Nos.
30 16-23).

II. Formulations and Methods for Administering Therapeutic Agents

The morphogens may be provided to an individual by
5 any suitable means, preferably directly (e.g., locally,
as by injection or topical administration to a tissue
locus) or systemically (e.g., parenterally or orally).
Where the morphogen is to be provided parenterally,
such as by intravenous, subcutaneous, intramuscular,
10 intraorbital, ophthalmic, intraventricular,
intracranial, intracapsular, intraspinal,
intracisternal, intraperitoneal, buccal, rectal,
vaginal, intranasal or by aerosol administration, the
morphogen preferably comprises part of an aqueous
15 solution. The solution is physiologically acceptable
so that in addition to delivery of the desired
morphogen to the patient, the solution does not
otherwise adversely affect the patient's electrolyte
and volume balance. The aqueous medium for the
20 morphogen thus may comprise normal physiologic saline
(9.85% NaCl, 0.15M), pH 7-7.4. The aqueous solution
containing the morphogen can be made, for example, by
dissolving the protein in 50% ethanol containing
acetonitrile in 0.1% trifluoroacetic acid (TFA) or 0.1%
25 HCl, or equivalent solvents. One volume of the
resultant solution then is added, for example, to ten
volumes of phosphate buffered saline (PBS), which
further may include 0.1-0.2% human serum albumin (HSA).
The resultant solution preferably is vortexed
30 extensively. If desired, a given morphogen may be made
more soluble by association with a suitable molecule.
For example, association of the mature dimer with the
pro domain of the morphogen keeps the morphogen soluble
in physiological buffers. In fact, the endogenous
35 protein is thought to be transported in this form.

- Another molecule capable of enhancing solubility and particularly useful for oral administrations, is casein. For example, addition of 0.2% casein increases solubility of the mature active form of OP-1 by 80%.
- 5 Other components found in milk and/or various serum proteins also may be useful.

- Useful solutions for parenteral administration may be prepared by any of the methods well known in the pharmaceutical art, described, for example, in Remington's Pharmaceutical Sciences (Gennaro, A., ed.), Mack Pub., 1990. Formulations may include, for example, polyalkylene glycols such as polyethylene glycol, oils of vegetable origin, hydrogenated
- 15 naphthalenes, and the like. Formulations for direct administration, in particular, may include glycerol and other compositions of high viscosity to help maintain the morphogen at the desired locus. Biocompatible, preferably bioresorbable, polymers, including, for
- 20 example, hyaluronic acid, collagen, tricalcium phosphate, polybutyrate, lactide and glycolide polymers, and lactide/glycolide copolymers, may be useful excipients to control the release of the morphogen in vivo. Other potentially useful parenteral
- 25 delivery systems for these morphogens include ethylene-vinyl acetate copolymer particles, osmotic pumps, implantable infusion systems, and liposomes. Formulations for inhalation administration contain as excipients, for example, lactose, or may be aqueous
- 30 solutions containing, for example, polyoxyethylene-9-lauryl ether, glycocholate and deoxycholate, or oily solutions for administration in the form of nasal drops, or as a gel to be applied intranasally.

Formulations for parenteral administration may also include glycocholate for buccal administration, methoxysalicylate for rectal administration, or citric acid for vaginal administration.

5

Suppositories for rectal administration also may be prepared by mixing the morphogen or morphogen-stimulating agent with a non-irritating excipient such as cocoa butter or other compositions which are solid at room temperature and liquid at body temperatures.

Formulations for topical administration to the skin surface may be prepared by dispersing the morphogen or morphogen-stimulating agent with a dermally acceptable carrier such as a lotion, cream, ointment or soap. Particularly useful are carriers capable of forming a film or layer over the skin to localize application and inhibit removal. For topical administration to internal tissue surfaces, the morphogen may be dispersed in a liquid tissue adhesive or other substance known to enhance adsorption to a tissue surface. For example, hydroxypropylcellulose or fibrinogen/thrombin solutions may be used to advantage. Alternatively, tissue-coating solutions, such as pectin-containing formulations, may be used.

Alternatively, the morphogens described herein may be administered orally. Oral administration of proteins as therapeutics generally is not practiced as most proteins are readily degraded by digestive enzymes and acids in the mammalian digestive system before they can be absorbed into the bloodstream. However, the morphogens described herein typically are acid stable and protease-resistant (see, for example, U.S. Pat.No. 4,968,590.) In addition, at least one morphogen, OP-1,

has been identified in mammary gland extract, colostrum and 57-day milk. Moreover, the OP-1 purified from mammary gland extract is morphogenically active. Specifically, this protein induces endochondral bone formation in mammals when implanted subcutaneously in association with a suitable matrix material, using a standard in vivo bone assay, such as is disclosed in U.S. Pat.No. 4,968,590. Moreover, the morphogen also is detected in the bloodstream. Finally, soluble form morphogen, e.g., mature morphogen associated with the pro domain, is morphogenically active. These findings indicate that oral and parenteral administration are viable means for administering morphogens to an individual. In addition, while the mature forms of certain morphogens described herein typically are sparingly soluble, the morphogen form found in milk (and mammary gland extract and colostrum) is readily soluble, probably by association of the mature, morphogenically active form with part or all of the pro domain of the intact sequence and/or by association with one or more milk components. Accordingly, the compounds provided herein also may be associated with molecules capable of enhancing their solubility in vitro or in vivo.

25

Where the morphogen or morphogen-stimulating agent comprises part of a tissue or organ preservation solution, any commercially available preservation solution may be used to advantage. For example, useful solutions known in the art include Collins solution, Wisconsin solution, Belzer solution, Eurocollins solution and lactated Ringer's solution. Generally, an organ preservation solution usually possesses one or more of the following properties: (a) an osmotic pressure substantially equal to that of the inside of a

35

mammalian cell, (solutions typically are hyperosmolar and have K⁺ and/or Mg⁺⁺ ions present in an amount sufficient to produce an osmotic pressure slightly higher than the inside of a mammalian cell; (b) the solution typically is capable of maintaining substantially normal ATP levels in the cells; and (c) the solution usually allows optimum maintenance of glucose metabolism in the cells. Organ preservation solutions also may contain anticoagulants, energy sources such as glucose, fructose and other sugars, metabolites, heavy metal chelators, glycerol and other materials of high viscosity to enhance survival at low temperatures, free oxygen radical inhibiting agents and a pH indicator. A detailed description of preservation solutions and useful components may be found, for example, in US Patent No. 5,002,965, the disclosure of which is incorporated herein by reference.

The compounds provided herein also may be associated with molecules capable of targeting the morphogen or morphogen-stimulating agent to the desired tissue. For example, an antibody, antibody fragment, or other binding protein that interacts specifically with a surface molecule on cells of the desired tissue, may be used. Useful targeting molecules may be designed, for example, using the single chain binding site technology disclosed, for example, in U.S. Pat. No. 5,091,513.

As described above, the morphogens provided herein share significant sequence homology in the C-terminal active domains. By contrast, the sequences typically diverge significantly in the sequences which define the pro domain. Accordingly, the pro domain is thought to

be morphogen-specific. As described above, it is also known that the various morphogens identified to date are differentially expressed in the different tissues. Accordingly, without being limited to any given theory, it is likely that, under natural conditions in the body, selected morphogens typically act on a given tissue. Accordingly, part or all of the pro domains which have been identified associated with the active form of the morphogen in solution, may serve as targeting molecules for the morphogens described herein. For example, the pro domains may interact specifically with one or more molecules at the target tissue to direct the morphogen associated with the pro domain to that tissue. Accordingly, another useful targeting molecule for targeting morphogen to a tissue of interest is part or all of a morphogen pro domain. For example, part or all of the pro domain of GDF-1 may be used to target a morphogen to nerve tissue. Alternatively, part or all of the pro domain of OP-1 or CBMP2 may be used to target a morphogen to bone tissue, both of which proteins are found naturally associated with bone tissue.

The morphogens described herein are useful for providing neuroprotective effects to alleviate neural pathway damage associated with the body's immune/inflammatory response to an initial injury to nerve tissue. As used herein, a "neural pathway" describes a nerve circuit for the passage of electric signals from a source to a target cell site and includes both the central nervous system (CNS) and peripheral nervous system (PNS). The pathway includes the neurons through which the electric impulse is transported, including groups of interconnecting neurons, the nerve fibers formed by bundled neuronal

axons, and the glial cells surrounding and associated with the neurons. An inflammatory response to nerve tissue injury may follow trauma to nerve tissue, caused, for example, by an autoimmune (including autoantibody) dysfunction, neoplastic lesion, infection, chemical or mechanical trauma, or other disease. An exemplary nerve-related inflammatory disease is multiple sclerosis. Neural pathway damage also can result from a reduction or interruption, e.g., occlusion, of a neural blood supply, as in an embolic stroke, (e.g, ischemia or hypoxia-induced injury), or by other trauma to the nerve or surrounding material. In addition, at least part of the damage associated with a number of primary brain tumors also appears to be immunologically related. Application of the morphogen directly to the cells to be treated, or providing the morphogen to the mammal systemically, for example, intravenously or indirectly by oral administration, may be used to alleviate and/or inhibit the immunologically related response to a neural injury. Alternatively, administration of an agent capable of stimulating morphogen expression and/or secretion in vivo, preferably at the site of injury, also may be used. Where the injury is to be induced, as during surgery or other aggressive clinical treatment, the morphogen or agent may be provided prior to induction of the injury to provide a neuroprotective effect to the nerve tissue at risk.

Where the morphogen is intended for use as a therapeutic to alleviate tissue damage associated with an immune/inflammatory condition of the CNS, an additional problem must be addressed: overcoming the so-called "blood-brain barrier", the brain capillary wall structure that effectively screens out all but

s lected categories of molecules present in the blood, preventing their passage into the brain. The blood-brain barrier may be bypassed effectively by direct infusion of the morphogen or morphogen-stimulating agent into the brain. Alternatively, the morphogen or morphogen-stimulating agent may be modified to enhance its transport across the blood-brain barrier. For example, truncated forms of the morphogen or a morphogen-stimulating agent may be most successful. Alternatively, the morphogen or morphogen-stimulating agent may be modified to render it more lipophilic, or it may be conjugated to another molecule which is naturally transported across the barrier, using standard means known to those skilled in the art, as, for example, described in Pardridge, Endocrine Reviews 7:314-330 (1986) and U.S. Pat. No. 4,801,575.

Finally, the morphogens or morphogen-stimulating agents provided herein may be administered alone or in combination with other molecules known to be beneficial in the treatment compositions and methods described herein, including, but not limited to anticoagulants, free oxygen radical inhibiting agents, salicylic acid, vitamin D, and other antiinflammatory agents. Psoriasis treatments also may include ultra-violet light treatment, zinc oxide and retinoids.

The compounds provided herein can be formulated into pharmaceutical compositions by admixture with pharmaceutically acceptable nontoxic excipients and carriers. As noted above, such compositions may be prepared for parenteral administration, particularly in

the form of liquid solutions or suspensions; for oral administration, particularly in the form of tablets or capsules; or intranasally, particularly in the form of powders, nasal drops, or aerosols.

5

The compositions can be formulated for parenteral or oral administration to humans or other mammals in therapeutically effective amounts, e.g., amounts which provide appropriate concentrations for a time
10 sufficient to alleviate the tissue destructive effects associated with the inflammatory response, including protecting tissue in anticipation of tissue damage.

As will be appreciated by those skilled in the art,
15 the concentration of the compounds described in a therapeutic composition will vary depending upon a number of factors, including the dosage of the drug to be administered, the chemical characteristics (e.g., hydrophobicity) of the compounds employed, and the
20 route of administration. The preferred dosage of drug to be administered also is likely to depend on such variables as the type and extent of progression of the tissue damage, the overall health status of the particular patient, the relative biological efficacy of
25 the compound selected, the formulation of the compound excipients, and its route of administration. In general terms, the compounds of this invention may be provided in an aqueous physiological buffer solution containing about 0.001% to 10% w/v compound for parenteral
30 administration. Typical dose ranges are from about 10 ng/kg to about 1 g/kg of body weight per day; a preferred dose range is from about 0.1 µg/kg to 100 mg/kg of body weight per day. Optimally, the morphogen dosage given is between 0.1-100 µg of protein
35 per kilogram weight of the patient. No obvious

morphogen induced pathological lesions are induced when mature morphogen (e.g., OP-1, 20 μ g) is administered daily to normal growing rats for 21 consecutive days. Moreover, 10 μ g systemic injections of morphogen (e.g., OP-1) injected daily for 10 days into normal newborn mice does not produce any gross abnormalities.

In administering morphogens systemically in the methods of the present invention, preferably a large volume loading dose is used at the start of the treatment. The treatment then is continued with a maintenance dose. Further administration then can be determined by monitoring at intervals the levels of the morphogen in the blood.

Where tissue injury is induced deliberately as part of, for example, a surgical procedure, the morphogen preferably is provided just prior to, or concomitant with induction of the trauma. Preferably, the morphogen is administered prophylactically in a surgical setting.

Alternatively, an effective amount of an agent capable of stimulating endogenous morphogen levels may be administered by any of the routes described above. For example, an agent capable of stimulating morphogen production and/or secretion from cells of affected tissue and/or transplant tissue may be provided to a mammal, e.g., by direct administration of the agent to the tissue to be treated. A method for identifying and testing agents capable of modulating the levels of endogenous morphogens in a given tissue is described generally herein in Example 15, and in detail in copending USSN 752,859, filed August 30, 1991, the disclosure of which is incorporated herein by reference. Briefly, candidate compounds can be

identified and tested by incubating the compound in vitro with a test tissue or cells thereof, for a time sufficient to allow the compound to affect the production, i.e., the expression and/or secretion, of a morphogen produced by the cells of that tissue.

For purposes of the present invention, the above-described morphogens effective in alleviating tissue damage associated with ischemic-reperfusion injury (or the agents that stimulate them, referred to collectively herein as "therapeutic agent") are administered prior to or during the restoration of oxygen (e.g., restoration of blood flow, reperfusion.) Where treatment is to follow an existing injury, the therapeutic agent preferably is administered as an intravenous infusion provided acutely after the hypoxic or ischemic condition occurs. For example, the therapeutic agent can be administered by intravenous infusion immediately after a cerebral infarction, a myocardial infarction, asphyxia, or a cardiopulmonary arrest. Where ischemia or hypoxia injury is deliberately and/or unavoidably induced as part of, for example, a surgical procedure where circulation to an organ or organ system is deliberately and/or transiently interrupted, e.g., in carotid enterectomy, coronary artery bypass, grafting, organ transplanting, fibrinolytic therapy, etc., the therapeutic agent preferably is provided just prior to, or concomitant with, reduction of oxygen to the tissue. Preferably, the morphogen is administered prophylactically in a surgical setting.

Similarly, where hyperoxia-induced injury already has occurred, the morphogen is administered upon diagnosis. Where hyperoxia injury may be induced as,

for exampl , during treatment of prematurely newborn babies, or patients suffering from pulmonary diseases such as emphysema, the therapeutic agent preferably is administered prior to administration of oxygen e.g., prophylactically.

III. Examples

10 Example 1. Identification of Morphogen-Expressing Tissue

Determining the tissue distribution of morphogens may be used to identify different morphogens expressed in a given tissue, as well as to identify new, related morphogens. Tissue distribution also may be used to identify useful morphogen-producing tissue for use in screening and identifying candidate morphogen-stimulating agents. The morphogens (or their mRNA transcripts) readily are identified in different tissues using standard methodologies and minor modifications thereof in tissues where expression may be low. For example, protein distribution may be determined using standard Western blot analysis or immunofluorescent techniques, and antibodies specific to the morphogen or morphogens of interest. Similarly, the distribution of morphogen transcripts may be determined using standard Northern hybridization protocols and transcript-specific probes.

30 Any probe capable of hybridizing specifically to a transcript, and distinguishing the transcript of interest from other, related transcripts may be used. Because the morphogens described herein share such high sequence homology in their active, C-terminal domains,

the tissue distribution of a specific morphogen transcript may best be determined using a probe specific for the pro region of the immature protein and/or the N-terminal region of the mature protein.

- 5 Another useful sequence is the 3' non-coding region flanking and immediately following the stop codon. These portions of the sequence vary substantially among the morphogens of this invention, and accordingly, are specific for each protein. For example, a particularly
- 10 useful Vgr-1-specific probe sequence is the PvuII-SacI fragment, a 265 bp fragment encoding both a portion of the untranslated pro region and the N-terminus of the mature sequence (see Lyons et al. (1989) PNAS 86:4554-4558 for a description of the cDNA sequence).
- 15 Similarly, particularly useful mOP-1-specific probe sequences are the BstXI-BglI fragment, a 0.68 Kb sequence that covers approximately two-thirds of the mOP-1 pro region; a StuI-StuI fragment, a 0.2 Kb sequence immediately upstream of the 7-cysteine domain;
- 20 and the EarI-PstI fragment, an 0.3 Kb fragment containing a portion of the 3'untranslated sequence (See Seq. ID No. 18, where the pro region is defined essentially by residues 30-291.) Similar approaches may be used, for example, with hOP-1 (Seq. ID No. 16)
- 25 or human or mouse OP-2 (Seq. ID Nos. 20 and 22.)

Using these morphogen-specific probes, which may be synthetically engineered or obtained from cloned sequences, morphogen transcripts can be identified in

30 mammalian tissue, using standard methodologies well known to those having ordinary skill in the art. Briefly, total RNA is prepared from various adult murine tissues (e.g., liver, kidney, testis, heart, brain, thymus and stomach) by a standard methodology

35 such as by the method of Chomczyaski et al. ((1987)

Anal. Biochem 162:156-159) and described below. Poly (A)+ RNA is prepared by using oligo (dT)-cellulose chromatography (e.g., Type 7, from Pharmacia LKB Biotechnology, Inc.). Poly (A)+ RNA (generally 15 µg) from each tissue is fractionated on a 1% agarose/formaldehyde gel and transferred onto a Nytran membrane (Schleicher & Schuell). Following the transfer, the membrane is baked at 80°C and the RNA is cross-linked under UV light (generally 30 seconds at 1 mW/cm²). Prior to hybridization, the appropriate probe is denatured by heating. The hybridization is carried out in a lucite cylinder rotating in a roller bottle apparatus at approximately 1 rev/min for approximately 15 hours at 37°C using a hybridization mix of 40% formamide, 5 x Denhardts, 5 x SSPE, and 0.1% SDS. Following hybridization, the non-specific counts are washed off the filters in 0.1 x SSPE, 0.1% SDS at 50°C.

Examples demonstrating the tissue distribution of various morphogens, including Vgr-1, OP-1, BMP2, BMP3, BMP4, BMP5, GDF-1, and OP-2 in developing and adult tissue are disclosed in co-pending USSN 752,764, and in Ozkaynak, et al., (1991) Biochem. Biophys. Res. Commn. 179:116-123, and Ozkaynak, et al. (1992) (JBC, in press), the disclosures of which are incorporated herein by reference. Using the general probing methodology described herein, northern blot hybridizations using probes specific for these morphogens to probe brain, spleen, lung, heart, liver and kidney tissue indicate that kidney-related tissue appears to be the primary expression source for OP-1, with brain, heart and lung tissues being secondary sources. OP-1 mRNA also was identified in salivary glands, specifically rat parotid glands, using this probing methodology. Lung tissue appears to be the

primary tissue expression source for Vgr-1, BMP5, BMP4 and BMP3. Lower levels of Vgr-1 also are seen in kidney and heart tissue, while the liver appears to be a secondary expression source for BMP5, and the spleen appears to be a secondary expression source for BMP4. GDF-1 appears to be expressed primarily in brain tissue. To date, OP-2 appears to be expressed primarily in early embryonic tissue. Specifically, northern blots of murine embryos and 6-day post-natal animals shows abundant OP2 expression in 8-day embryos. Expression is reduced significantly in 17-day embryos and is not detected in post-natal animals.

Example 2. Active Morphogens in Body Fluids

OP-1 expression has been identified in saliva (specifically, the rat parotid gland, see Example 1), human blood serum, and various milk forms, including mammary gland extract, colostrum, and 57-day bovine milk. Moreover, and as described in USSN 923,780, the disclosure of which is incorporated herein by reference, the body fluid-extracted protein is morphogenically active. The discovery that the morphogen naturally is present in milk and saliva, together with the known observation that mature, active OP-1 is acid-stable and protease-resistant, indicate that oral administration is a useful route for therapeutic administration of morphogen to a mammal. Oral administration typically is the preferred mode of delivery for extended or prophylactic therapies. In addition, the identification of morphogen in all milk forms, including colostrum, suggests that the protein may play a significant role in tissue development, including skeletal development, of juveniles.

2.1 Morphogen Detection in Milk

OP-1 was partially purified from rat mammary gland extract and bovine colostrum and 57 day milk by passing
5 these fluids over a series of chromatography columns:
(e.g., cation-exchange, affinity and reverse phase). At
each step the eluant was collected in fractions and
these were tested for the presence of OP-1 by standard
immunoblot. Immunoreactive fractions then were
10 combined and purified further. The final, partially
purified product then was examined for the presence of
OP-1 by Western blot analysis using OP-1-specific
antisera, and tested for in vivo and in vitro activity.

15 OP-1 purified from the different milk sources were
characterized by Western blotting using antibodies
raised against OP-1 and BMP2. Antibodies were prepared
using standard immunology protocols well known in the
art, and as described generally in Example 15, below,
20 using full-length E. coli-produced OP-1 and BMP2 as the
immunogens. In all cases, the purified OP-1 reacted
only with the anti-OP-1 antibody, and not with
anti-BMP2 antibody.

25 The morphogenic activity of OP-1 purified from
mammary gland extract was evaluated in vivo essentially
following the rat model assay described in U.S. Pat.
No. 4,968,590, hereby incorporated by reference.
Briefly, a sample was prepared from each OP-1
30 immunoreactive fraction of the mammary gland
extract-derived OP-1 final product by lyophilizing a
portion (33%) of the fraction and resuspending the
protein in 220 μ l of 50% acetonitrile/0.1% TFA. After
vortexing, 25 mg of collagen matrix was added. The
35 samples were lyophilized overnight, and implanted in

Long Evans rats (Charles River Laboratories, Wilmington, MA, 28-35 days old). Each fraction was implanted in duplicate. For details of the collagen matrix implantation procedure, see, for example, U.S. Pat. No. 4,968,590, hereby incorporated by reference. After 12 days, the implants were removed and evaluated for new bone formation by histological observation as described in U.S. Patent No. 4,968,590. In all cases, the immunoreactive fractions were osteogenically active.

2.2 Morphogen Detection in Serum

Morphogen may be detected in serum using morphogen-specific antibodies. The assay may be performed using any standard immunoassay, such as Western blot (immunoblot) and the like. Preferably, the assay is performed using an affinity column to which the morphogen-specific antibody is bound and through which the sample serum then is poured, to selectively extract the morphogen of interest. The morphogen then is eluted. A suitable elution buffer may be determined empirically by determining appropriate binding and elution conditions first with a control (e.g., purified, recombinantly-produced morphogen.) Fractions then are tested for the presence of the morphogen by standard immunoblot, and the results confirmed by N-terminal sequencing. Preferably, the affinity column is prepared using monoclonal antibodies. Morphogen concentrations in serum or other fluid samples then may be determined using standard protein quantification techniques, including by spectrophotometric absorbance or by quantitation of conjugated antibody.

Presented below is a sample protocol for identifying OP-1 in serum. Following this general methodology other morphogens may be detected in body fluids, including serum. The identification of morphogen in serum further indicates that systemic administration is a suitable means for providing therapeutic concentrations of a morphogen to an individual, and that morphogens likely behave systemically as endocrine-like factors. Finally, using this protocol, fluctuations in endogenous morphogen levels can be detected, and these altered levels may be used as an indicator of tissue dysfunction. Alternatively, fluctuations in morphogen levels may be assessed by monitoring morphogen transcription levels, either by standard northern blot analysis as described in Example 1, or by in situ hybridization, using a labelled probe capable of hybridizing specifically to morphogen mRNA, and standard RNA hybridization protocols well described in the art and described generally in Example 1.

OP-1 was detected in human serum using the following assay. A monoclonal antibody raised against mammalian, recombinantly produced OP-1 using standard immunology techniques well described in the art and described generally in Example 15, was immobilized by passing the antibody over an agarose-activated gel (e.g., Affi-GelTM, from Bio-Rad Laboratories, Richmond, CA, prepared following manufacturer's instructions) and used to purify OP-1 from serum. Human serum then was passed over the column and eluted with 3M K-thiocyanate. K-thiocyanate fractions then were dialyzed in 6M urea, 20mM PO₄, pH 7.0, applied to a C8 HPLC column, and eluted with a 20 minute, 25-50% acetonitrile/0.1% TFA gradient. Mature, recombinantly

produced OP-1 homodimers elute between 20-22 minutes. Fractions then were collected and tested for the presence of OP-1 by standard immunoblot using an OP-1 specific antibody as for Example 2.A.

5

Administered or endogenous morphogen levels may be monitored in the therapies described herein by comparing the quantity of morphogen present in a body fluid sample with a predetermined reference value, for example, to evaluate the efficiency of a therapeutic protocol, and the like. In addition, fluctuations in the level of endogenous morphogen antibodies may be detected by this method, most likely in serum, using an antibody or other binding protein capable of interacting specifically with the endogenous morphogen antibody. Detected fluctuations in the levels of the morphogen or endogenous antibody may be used, for example, as indicators of a change in tissue status. For example, as damaged tissue is regenerated and the tissue or organ's function returns to "normal" and, in the absence of additional tissue damage, lower doses of morphogen may be required, and a higher level of circulating morphogen antibody may be measured.

25 Example 3. Effect of Morphogen after the Onset of the Ischemic Process

The cardioprotective effect of morphogens following ischemic-reperfusion injury in a mammal can readily be assessed in a rat model. In this example, morphogen (e.g., OP-1) is administered just prior to the onset of the ischemic process in experimentally-induced myocardial infarcted rats, essentially following the method of Lefer, et al. (1990) Science 249:61-64 and (1992) J. Mol. Cell. Cardiol. 24: 385-393, the

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disclosures of which are hereby incorporated by reference. Briefly, loss of myocardial tissue function following ischemia and reperfusion is assayed by measuring loss of myocardial creatine kinase activity (CK) and loss of endothelium-dependent vasorelaxation function (see Example 4, below).

In a first group of ether-anesthetized rats, the left coronary artery was occluded just proximal to the first main branch with a silk ligature to induce a myocardial infarction (MI). The ligature was removed 10 minutes after occlusion to allow for coronary reperfusion. This first group is referred to herein as the "myocardial infarcted" (MI) group. A second group of rats underwent the same procedure except that the coronary artery was not occluded, and thus no myocardial infarction occurred. The second group of rats is referred to herein as the "sham myocardial infarcted group" (SHAM MI).

The first group of rats, the MI group of rats, further was divided into three sub-groups. 2 μ g of morphogen (OP-1) were injected intravenously into the first sub-group of MI rats 10 minutes after ligature, immediately before reperfusion; into the second sub-group of MI rats 20 μ g of OP-1 were injected intravenously 10 minutes after ligature and immediately before reperfusion; and into the third sub-group of MI rats (control) was injected vehicle only, e.g., 0.9% NaCl, as for the OP-1 treated rats.

Twenty-four hours later, the hearts were removed from all of the rats and the levels of creatine kinase (CK) from the left ventricle (the infarcted region) and from the interventricular septum (the control

nonischemic region) were determined by standard means. By comparing the difference in CK activities in both regions, the amount of CK activity lost from the infarcted region was used as an index of cardiac cellular injury to the infarcted region.

As shown in Figure 1, the data indicate that morphogens (e.g., OP-1) can provide significant cardioprotective effect when provided to ischemic tissue. In the figure, CK loss is graphed as the difference in specific CK activity between the interventricular septum and the left ventricle.

The loss of CK activity by the subgroup of MI rats which received 2 μ g of OP-1 just before reperfusion showed some protection as compared with the control MI rats which received injections of vehicle alone, when the levels from both subgroups are measured against, and compared to, the levels obtained for the SHAM MI control. Significant cardioprotection was observed in the subgroup of MI rats which received 20 μ g of OP-1 immediately before reperfusion as compared with the control MI rats which received injections of vehicle alone, when the levels from both subgroups are measured against, and compared to, the levels contained within the SHAM MI control.

These data indicate that OP-1 offers significant cardiac protection when administered after ischemia and before reperfusion.

A variation of this example also may be performed providing morphogen to the animal prior to induction of ischemia. The experiments may be performed both in normal and immune-compromised rats to assess the cardioprotective effects of morphogen administered prior to ischemia.

Example 4. Vasodilation of Myocardial Infarcted Cardiac Tissue Treated with Morphogen

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Certain vasodilators like acetylcholine (ACh) and adenosine diphosphate (ADP, an immune mediator) exert their vasodilation activity only in the presence of intact endothelium, which is stimulated to release a substance termed endothelium-derived relaxing factor (EDRF). If the endothelium is injured so that EDRF is not released, no vasodilation occurs in response to these endothelium-dependent agents. In contrast, several other vasodilators including nitroglycerine (NTG) and nitroprusside, are endothelium-independent dilators, as they dilate blood vessels directly.

The present example demonstrates the ability of OP-1 to prevent the loss of cardioendothelium-dependent relaxation (EDR) activity in the coronary microvasculature following reperfusion of ischemic myocardium, and their ability to reduce myocardial injury 24 hours after morphogen treatment. Briefly, 2 or 24 hours after morphogen treatment ischemia-reperfusion injury is induced in isolated rat hearts, the reperfused hearts are vasodilated with either ACh or NTG. In the absence of morphogen treatment, injured tissue should inhibit ACh-induced vasodilation, but not NTG-induced vasodilation. Morphogen treatment is expected to enhance ACh-induced vasodilation in the reperfused hearts.

Accordingly, 48 adult male Sprague-Dawley rats (250-330 g) were divided into eight groups of 6 rats each. Twelve rats were subjected to sham myocardial infarcts (SHAM MI) as described in Example 3. The hearts of the remaining 36 rats were isolated as follows: one set of twelve rats was injected intravenously with OP-1 24 hours prior to isolation of the heart; another set of rats was injected intravenously with 20 µg of OP-1 2 hours prior to isolation of the heart; the final group of rats was injected with vehicle only (e.g., 0.9% NaCl.). The rats then were anesthetized with pentobarbital sodium (35 mg/kg, intraperitoneal); their hearts were isolated and perfused by the Langendorff method at a constant flow (15 ml/min) with oxygenated Krebs-Henseleit solution (Aoki et al. (1988) J. Pharmacol. 95:35).

Each group of rats then were divided into two subgroups of six rats each. Twenty minutes before reperfusion, coronary vasodilator response was measured by inducing constriction with 0.05 µmol U-44619 (9,11-methanoepoxyprostaglandin H₂) followed by a vasodilating agent 3 minutes later: subgroup one - 15 nmol ACh; subgroup 2 - 15 nmol NTG and the increase in coronary perfusion pressure (CPP) level measured as an indication of vasodilation. When CPP levels returned to normal, the hearts were subjected to ischemia by reducing coronary infusion to 15% of control flow for 30 minutes, then reestablishing normal flow, i.e., reperfusion, for an additional 20 minutes.

30

The vasodilator response then was remeasured by constriction and administration of vasodilating agent as described above.

The results of these experiments are shown in FIG 2. Before the ischemic event, both ACh and NTG gave normal vasorelaxant results in all events. The hearts which received OP-1 24 hours prior to ischemia showed an approximately 70% response to ACh while the hearts which received OP-1 2 hours prior to ischemia showed a 55% response to ACh. The group which received vehicle alone showed a 40% response to ACh. Finally, the control group which was not subjected to ischemia showed an ACh response of approximately 95%. This shows that endothelium-dependent vasodilators exert a reduced vasodilator response following ischemia and reperfusion in the rat heart. Moreover, OP-1 significantly preserved endothelium-dependent dilation when provided 24 hours prior to induction of myocardial ischemia. No defect in vasodilation occurred in response to the direct vasodilator (NTG); NTG-induced vasodilation activities were 95% of initial in hearts subject to ischemia and 100% of initial nonischemic hearts.

Example 5. Effect of Morphogen on Neutrophil Adherence

The role of neutrophil adherence in endothelium dysfunction and the cardioprotective effects of morphogens in modulating this activity can be assessed using a standard polymorphonuclear neutrophil (PMN) adherence assay such as described in Lefer et al., (1992) J. Mol. Cell. Cardiol. 24: 385-393, disclosed hereinabove by reference. Briefly, segments of superior mesenteric artery were isolated from rats which had either been treated with morphogen (OP-1, 20 µg) or 0.9% NaCl, 24 h prior to isolation of the artery. The segments were cleaned, cut into transverse rings of 1-2mm in length, and these were subsequently

cut open and incubated in K-H solution at 37°C, pH 7.4. Neutrophils were prepared and fluorescently labelled using standard procedures (e.g., leukocytes were isolated from rats essentially following the procedure of Pertroft et. al. (1968) Exp Cell Res 50: 355-368, washed in phosphate buffered saline (PBS), purified by gradient centrifugation; and labelled by the method of Yuan et. al. (1990) Microvasc Res 40: 218-229..

10 Labelled neutrophils then were added to open ring baths and activated with 100nM leukotriene B₄ (LTB₄). Rings were incubated for 20 minutes and the number of neutrophils adhering to the endothelial surface then determined visually by fluorescent microscopy.

15 As shown in Figure 3, unstimulated PMNs (i.e., PMNs alone) added to the baths did not significantly adhere to the vascular endothelium. In rings taken from rats injected with 0.9% NaCl, activation of neutrophils with LTB₄ (100 nM) greatly increased the number of PMNs adherent to the endothelium (P<0.001). OP-1 (20 µg administered 24 h prior) significantly inhibited adherence of PMNs activated by LTB₄ (P<0.01 from control).

25 Example 6. In Vivo Models for Ischemic-Reperfusion Protection in Lung, Nerve and Renal Tissue.

30 Other tissues seriously affected by ischemic-reperfusion injury include neural tissue, renal tissue and lung tissue. The effect of morphogens on alleviating the ischemic-reperfusion injury in these tissues may be assessed using methodologies and models known to those skilled in the art, and disclosed below.

35

Similarly, a methodology also is provided for assessing the tissue-protective effects of a morphogen on damaged lung tissue following hyperoxia injury.

5 For example, the rabbit embolic stroke model provides a useful method for assessing the effect of morphogens on tissue injury following cerebral ischemia-reperfusion. The protocol disclosed below is essentially that of Phillips et al. (1989) Annals of
10 Neurology 25:281-285, the disclosure of which is herein incorporated by reference. Briefly, white New England rabbits (2-3kg) are anesthetized and placed on a respirator. The intracranial circulation then is selectively catheterized by the Seldinger technique.
15 Baseline cerebral angiography then is performed, employing a digital substration unit. The distal internal carotid artery or its branches then is selectively embolized with 0.035 ml of 18-hour-aged autologous thrombus. Arterial occlusion is documented
20 by repeat angiography immediately after embolization. After a time sufficient to induce cerebral infarcts (15 minutes or 90 minutes), reperfusion is induced by administering a bolus of a reperfusion agent such as the TPA analogue Fb-FB-CF (e.g., 0.8 mg/kg over 2
25 minutes).

The effect of morphogen on cerebral infarcts can be assessed by administering varying concentrations of morphogens, e.g., OP1, at different times preceding or
30 following embolization and/or reperfusion. The rabbits are sacrificed 3-14 days post embolization and their brains prepared for neuropathological examination by fixing by immersion in 10% neutral buffered formalin

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for at least 2 weeks. The brains then are sectioned in a coronal plane at 2-3 mm intervals, numbered and submitted for standard histological processing in paraffin, and the degree of neutral tissue necrosis determined visually.

The renal-protective effects of morphogens on renal ischemia-reperfusion injury readily can be assessed using the mouse model disclosed by Ouellette, et al. (1990), J. Clin. Invest. 85:766-771, the disclosure of which is hereby incorporated by reference. Briefly, renal ischemia is induced surgically in 35-45 days old out-bred Swiss male mice by performing a standard right nephrectomy, and occluding the artery to the left kidney with a microaneurism clamp for 10-30 minutes. Morphogen then may be provided parentally, at various times prior to or following occlusion and/or reperfusion. The effects of morphogen then may be assessed by biological evaluation and histological evaluation using standard techniques well known in the art.

The tissue protective effects of morphogen on tissue exposed to lethally high oxygen concentrations may be assessed by the following procedure. Adult rats (275-300 gms) first are provided with morphogen (e.g., hOP1) or vehicle only, and then are exposed to 96-98% oxygen essentially as described by Rinaldo et al (1983) Am. Rev. Respir. Dis. 130:1065, to induce hyperoxia. Animals are housed in plastic cages (38 cm x 48 cm x 21 cm). A cage containing 4-5 animals is placed in a 75 liter water-sealed plexiglass chamber. An atmosphere of 96-98% oxygen then is maintained by delivery of O₂ gas (liquid O₂). Gas flow through the chamber is adjusted to maintain at least 10 air changes/hr.,

temperature at $22 \pm 1^\circ\text{C}$, minimal levels of condensation within the cage, and carbon dioxide concentration of $< 0.5\%$ as measured with a mass spectrophotometric medical gas analyzer.

5

At the end of 72 hours all survivors are observed at room air for 1.5 hours and at longer time periods to assess degree of respiratory distress and cyanosis induced by the initial insult and subsequent immune cell-mediated damage. The number of survivors at the end of the challenge is recorded and the treated groups compared with the untreated control group by chi-square test of proportions. Several of the surviving animals for each group are randomly chosen for histological processing of lung tissue.

15

Lung tissue for histological processing is fixed by infusion of 10% buffered formalin through a tracheal cannula at a constant pressure of 20 cm H_2O . After fixation for 24-48 hours, sections from each lobe are cut and subsequently stained with hematoxylin and eosin. Coded slides then are examined, preferably in a double-blind fashion for evidence of pathological changes such as edema, interstitial cellularity, and inflammatory response.

25

Example 7. Morphogen Inhibition of Cellular and Humoral Inflammatory Response

Morphogens described herein inhibit multinucleation of mononuclear phagocytic cells under conditions where these cells normally would be activated, e.g., in response to a tissue injury or the presence of a foreign substance. For example, in the absence of morphogen, an implanted substrate material (e.g.,

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implanted subcutaneously) composed of, for example, mineralized bone, a ceramic such as titanium oxide or any other substrate that provokes multinucleated giant cell formation, rapidly becomes surrounded by multinucleated giant cells, e.g., activated phagocytes stimulated to respond and destroy the foreign object. In the presence of morphogen however, the recruited cells remain in their mononuclear precursor form and the matrix material is undisturbed. Figure 4 illustrates this effect of morphogens, in a schematic representation of histology results of a titanium oxide substrate implanted subcutaneously. In the figure, "mg" means mononuclear giant cells and "ob" means osteoblasts. The substrate represented in Fig. 4B was implanted together with morphogen (OP-1) and newly formed osteoblasts are evident surrounding the substrate. By contrast, the substrate represented in Fig. 4A was implanted without morphogen and extensive multinucleated giant cell formation is evident surrounding the substrate. Accordingly, the morphogens' effect in inhibiting excessive bone mass loss in a mammal also may include inhibiting activation of these cells.

In addition, the morphogens described herein also suppress antibody production stimulated in response to a foreign antigen in a mammal. Specifically, when bovine bone collagen matrix alone was implanted in a bony site in a rat, a standard antibody response to the collagen is stimulated in the rat as determined by standard anti-bovine collagen ELISA experiments performed on blood samples taken at four week intervals following implantation (e.g., between 12 and 20 weeks.) Serum anti-collagen antibody titers, measured by ELISA essentially following the procedure described by

Nagler-Anderson et al, (1986) PNAS 83:7443-7446, the disclosure of which is incorporated herein by reference, increased consistently throughout the experiment. However, when the matrix was implanted together with a morphogen (e.g., OP-1, dispersed in the matrix and adsorbed thereto, essentially as described in U.S. Pat. No. 4,968,590) anti-bovine collagen antibody production was suppressed significantly. This ability of morphogen to suppress the humoral response is further evidence of morphogen utility in alleviating tissue damage associated with autoimmune diseases, including autoantibody diseases, such as rheumatoid arthritis.

15 Example 8. Morphogen protection of Gastrointestinal Tract Mucosa from Ulceration and Inflammation

Oral mucositis is a gastrointestinal tract inflammatory disease which involves ulcerations of the mouth mucosa as a consequence of, e.g., radiation therapy or chemotherapy. While not typically a chronic disease, the tissue destructive effects of oral mucositis mirror those of chronic inflammatory diseases such as IBD. The example below demonstrates morphogen efficacy in protecting the oral mucosa from oral mucositis in a hamster model, including both inhibiting inflammatory ulceration and enhancing regeneration of ulcerated tissue. Details of the protocol can be found in Sonis, et al., (1990) Oral Surg. Oral Med. Oral Pathol 69: 437-443, the disclosure of which is incorporated herein by reference. Based on these data,

the morphogens described herein should be efficacious in treating chronic inflammatory diseases including IBD, arthritis, psoriasis and psoriatic arthritis, multiple sclerosis, and the like.

5

Golden syrian hamsters (6-8 wks old; Charles River Laboratories, Wilmington, MA) were divided into 3 test groups: Group 1, a placebo (e.g., saline) control, and a morphogen low dose group (100 ng) and a morphogen
10 high dose group (1 μ g), Groups 2 and 3, respectively. Morphogen dosages were provided in 30% ethanol. Each group contained 12 animals.

Beginning on day 0 and continuing through day 5,
15 Groups 2 and 3 received twice daily morphogen applications. On day 3, all groups began the mucositis-induction procedure. 5-fluorouracil (60 mg/kg) was injected intraperitoneally on days 3 and 5. On day 7, the right buccal pouch mucosa was
20 superficially irritated with a calibrated 18 gauge needle. In untreated animals, severe ulcerative mucositis was induced in at least 80% of the animals by day 10.

25 For each administration of the vehicle control (placebo) or morphogen, administration was performed by first gently drying the cheek pouch mucosa, then providing an even application over the mucosal surface of the vehicle or morphogen material. A
30 hydroxypropylcellulose-based coating was used to maintain contact of the morphogen with the mucosa. This coating provided at least 4 hours of contact time.

On day 12, two animals in each group were sacrificed for histological studies. The right buccal pouch mucosa and underlying connective tissue were dissected and fixed in 10% formalin using standard
5 dissection and histology procedures. The specimens were mounted in paraffin and prepared for histologic examination. Sections then were stained with hematoxylin and eosin and were examined blindly by
10 three oral pathologists with expertise in hamster histology and scored blind against a standard mucositis panel. The extent of atrophy, cellular infiltration, connective tissue breakdown, degree of ulceration and epithelialization were assessed.

15 The mean mucositis score for each group was determined daily for each experimental group for a period of 21 days by photography and visual examination of the right buccal cheek pouch. Differences between groups were determined using a standard 't' test, e.g.,
20 the Students' 't' test. In addition, data was evaluated between groups by comparing the numbers of animals with severe mucositis using Chi Square statistical analysis. The significance of differences in mean daily weights also was determined.

25 The experimental results are presented in Fig. 5, which graphs the effect of morphogen (high dose, squares; low dose, diamonds) and placebo (circles) on mean mucositis scores. Both low and high morphogen
30 doses inhibit lesion formation significantly in a dose-dependent manner. In addition, histology results consistently showed significantly reduced amounts of

tissue atrophy, cellular debris, and immune effector cells, including macrophages and activated neutrophils, in the morphogen-treated animals, as compared with the untreated, control animals.

5

Example 9. Morphogen Effect on Fibrogenesis and Scar Tissue Formation

The morphogens described herein induce tissue morphogenesis of damaged or lost tissue. The ability of these proteins to regenerate new tissue enhances the anti-inflammatory effect of these proteins. Provided below are a series of in vitro experiments demonstrating the ability of morphogens to induce migration and accumulation of mesenchymal cells. In addition, the experiments demonstrate that morphogens, unlike TGF- β , do not stimulate fibrogenesis or scar tissue formation. Specifically, morphogens do not stimulate production of collagen, hyaluronic acid (HA) or metalloproteinases in primary fibroblasts, all of which are required for fibrogenesis or scar tissue formation. By contrast, TGF- β , a known inducer of fibrosis, but not of tissue morphogenesis, does stimulate production of these fibrosis markers.

25

Chemotaxis and migration of mesenchymal progenitor cells were measured in modified Boyden chambers essentially as described by Fava, R.A. et al (1991) J. Exp. Med. 173: 1121-1132, the disclosure of which is incorporated herein by reference, using polycarbonate filters of 2, 3 and 8 micron pores to measure migration of progenitor neutrophils, monocytes and fibroblasts. Chemotaxis was measured over a range of morphogen concentrations, e.g., 10^{-20} M to 10^{-12} M OP-1. For progenitor neutrophils and monocytes, 10^{-18} - 10^{-17} M OP-1

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consistently induced maximal migration, and 10^{-14} to 10^{-13} M OP-1 maximally induced migration of progenitor fibroblasts. In all cases the chemotactic activity could be inhibited with anti-OP-1 antibody. Similar migration activities also were measured and observed with TGF- β .

The effect of morphogen on fibrogenesis was determined by evaluating fibroblast production of hyaluronic acid (HA), collagen, collagenase and tissue inhibitor of metalloproteinases (TIMP).

Human fibroblasts were established from explants of infant foreskins and maintained in monolayer culture using standard culturing procedures. (See, for example, (1976) J. Exp. Med. 144: 1188-1203.) Briefly, fibroblasts were grown in maintenance medium consisting of Eagle's MEM, supplemented with nonessential amino acids, ascorbic acid (50 μ g/ml), NaHCO_3 and HEPES buffers (pH 7.2), penicillin (100 U/ml), streptomycin (100 μ g/ml), amphotericin B (1 μ g/ml) and 9% heat inactivated FCS. Fibroblasts used as target cells to measure chemotaxis were maintained in 150 mm diameter glass petri dishes. Fibroblasts used in assays to measure synthesis of collagen, hyaluronic acid, collagenase and tissue inhibitors of metalloproteinases (TIMP) were grown in 100 mm diameter plastic tissue culture petri dishes.

The effects of morphogen on fibroblast production of hyaluronic acid, collagens, collagenase and TIMP were determined by standard assays (See, for example, Posttethwaite et al. (1989) J. Clin. Invest. 83: 629-636, Posttethwaite (1988) J. Cell Biol. 106: 311-318 and Clark et al (1985) Arch. Bio-chem Biophys. 241: 36-

44, the disclosures of which are incorporated by reference.) For these assays, fibroblasts were transferred to 24-well tissue culture plates at a density of 8×10^4 cells per well. Fibroblasts were grown confluency in maintenance medium containing 9% FCS for 72 h and then grown in serum-free maintenance medium for 24 h. Medium was then removed from each well and various concentrations of OP-1 (recombinantly produced mature or soluble form) or TGF- β -1 (R&D Systems, Minneapolis) in 50 μ l PBS were added to triplicate wells containing the confluent fibroblast monolayers. For experiments that measured production of collagenase and TIMP, maintenance medium (450 μ l) containing 5% FCS was added to each well, and culture supernatants were harvested from each well 48 h later and stored at -70°C until assayed. For experiments that assessed HA production, maintenance medium (450 μ l) containing 2.5% FCS was added to each well, and cultures grown for 48 h. For experiments that measured fibroblast production of collagens, serum-free maintenance medium (450 μ l) without non-essential amino acids was added to each well and cultures grown for 72 h. Fibroblast production of HA was measured by labeling newly synthesized glycosaminoglycans (GAG) with [^3H]-acetate the last 24 h of culture and quantitating released radioactivity after incubation with hyaluronidase from Streptomyces hyalurolyticus (ICN Biochemicals, Cleveland, OH) which specifically degrades hyaluronic acid. Production of total collagen by fibroblasts was measured using a collagenase-sensitive protein assay that reflects [^3H]-proline incorporation the last 24 h of culture into newly synthesized collagens. Collagenase and TIMP protein levels in fibroblast cultures supernatants was measured by specific ELISAs.

As shown in Fig. 6, OP1 does not stimulate significant collagen or HA production, as compared with TGF- β . In the figure, panel A shows OP-1 effect on collagen production, panel B shows TGF- β effect on collagen production, and panels C and D show OP-1 (panel C) and TGF- β (panel D) effect on HA production. The morphogen results were the same whether the soluble or mature form of OP1 was used. By contrast, the latent form of TGF- β (e.g., pro domain-associated form of TGF- β) was not active.

Example 10. Morphogen Inhibition of Epithelial Cell Proliferation

This example demonstrates the ability of morphogens to inhibit epithelial cell proliferation in vitro, as determined by ^3H -thymidine uptake using culture cells from a mink lung epithelial cell line (ATCC No. CCL 64), and standard mammalian cell culturing procedures. Briefly, cells were grown to confluency in Eagle's minimum essential medium (EMEM) supplemented with 10% fetal bovine serum (FBS), 200 units/ml penicillin, and 200 $\mu\text{g/ml}$ streptomycin, and used to seed a 48-well cell culture plate at a cell density of 200,000 cells per well. When this culture became confluent, the media was replaced with 0.5 ml of EMEM containing 1% FBS and penicillin/streptomycin and the culture incubated for 24 hours at 37 C. Morphogen test samples in EMEM containing 5% FBS then were added to the wells, and the cells incubated for another 18 hours. After incubation, 1.0 μCi of ^3H -thymidine in 10 μl was added to each well, and the cells incubated for four hours at 37 C. The media then was removed and the cells washed once with ice-cold phosphate-buffer saline and DNA precipitated by adding 0.5 ml of 10% TCA to each well

and incubating at room temperatur of 15 minutes. The cells then were washed three times with ice-cold distilled water, lysed with 0.5 ml 0.4 M NaOH, and the lysate from each well then transferred to a
 5 scintillation vial and the radioactivity recorded using a scintillation counter (Smith-Kline Beckman).

The results are presented in Table III, below. The anti-proliferative effect of the various morphogens
 10 tested was expressed as the counts of ³H-thymidine (x 1000) integrated into DNA, and were compared with untreated cells (negative control) and TGF- β (1 ng), a local-acting factor also known to inhibit epithelial cell proliferation. COP-5 and COP-7 are biosynthetic
 15 constructs that previously have been shown to have osteogenic activity, capable of inducing the complete cascade resulting in endochondral bone formation in a standard rat bone assay (see U.S. Pat. No. 5,011,691.) The morphogens significantly inhibit epithelial cell
 20 proliferation. Similar experiments, performed with the morphogens COP-16, bOP (bone-purified osteogenic protein, a dimeric protein comprising CBMP2 and OP-1), and recombinant OP-1, also inhibit cell proliferation. bOP and COP-16 also induce endochondral bone formation
 25 (see US Pat. No. 4,968,590 and 5,011,691.)

TABLE III

	<u>Thymidine uptake (x 1000)</u>
30 control	50.048, 53.692
COP-7-1 (10 ng)	11.874
COP-7-2 (3 ng)	11.136
COP-5-1 (66 ng)	16.094
COP-5-2 (164 ng)	14.43
35 TGF- β (1 ng)	1.86, 1.478

Example 11. Morphogen Treatment of a Systemic
Inflammatory Disease

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The following example provides a rat adjuvant-induced arthritis model for demonstrating morphogen efficacy in treating arthritis and other systemic inflammatory diseases. Rat adjuvant-induced arthritis induces a systemic inflammatory disease with bone and cartilage changes similar to those observed in rheumatoid arthritis, but in an accelerated time span (see, for example, Pearson (1964) Arth. Rheum. 7:80). A detailed description of the protocol is provided in Walz, et al., (1971) J. Pharmac. Exp. Ther. 178: 223-231, the disclosure of which is incorporated herein by reference.

Briefly, Sprague-Dawley female rats (e.g., Charles River Laboratories, Wilmington, MA) are randomized into 3 groups: control; morphogen, low dose (e.g., 1-10 $\mu\text{g/kg}$ weight per day) and morphogen, high dose (e.g., 10-20 $\mu\text{g/kg}$ weight per day), referred to as Groups 1, 2, and 3, respectively.

25

Adjuvant arthritis is induced in all three groups by injection of 0.05 ml of a suspension of 1.5% dead *Mycobacterium butyricum* in mineral oil into the subplantar surface of the right hand paw. On Day 18 after adjuvant injection, the limb volumes of both hind limb are determined. In the absence of morphogen treatment, a systemic arthritic condition is induced in adjuvant-injected rats by this time, as determined by significant swelling of the uninjected hind limbs (< 2.3 ml, volume measured by mercury displacement).

35

Subsequent determinations of paw edema and x-ray scores are made on the uninjected hind limb. Rats in Group 2 and 3 also are dosed orally daily, beginning on Day 1, with morphogen. Limb volumes are recorded on Days 29 and 50 after adjuvant injection and edema determined by volume difference compared to Day 18. The uninjected hind limb on each rat is x-rayed on Day 50 and the joint damage assayed on an arbitrary scale of 1 to 10 (1=no damage, 10=maximum damage). Data on differences between control and treated groups (Day 29 edema, Day 50 edema and Day 50 x-ray scores) are analyzed by using a standard "t-test. Morphogen-treated rats show consistently reduced joint damage (e.g., decreased in edema and in x-ray scores) as compared with untreated control rats.

As another, alternative example, Groups 2 and 3 are dosed daily with morphogen beginning on Day 18 and continuing through Day 50 to demonstrate the efficacy of morphogens in arthritic animals.

Example 12. Morphogen Inhibition of Localized Edema

The following example demonstrates morphogen efficacy in inhibiting a localized inflammatory response in a standard rat edema model. Experimental rats (e.g., Long-Evans from Charles River Laboratories, Wilmington, MA) are divided into three groups: Group 1, a negative control, which receives vehicle alone; Group 2, a positive control, to which is administered a well-known characterized anti-inflammatory agent (e.g., indomethacin), and Group 3, to which morphogen is provided.

Groups 2 and 3 may be further subdivided to test low, medium and high doses (e.g., Group 2: 1.0 mg/kg, 3.0 mg/kg and 9.0 mg/kg indomethacin; Group 3: 0.1-5 μ g; 5-20 μ g, and 20-50 μ g of morphogen). Sixty minutes after indomethacin or morphogen is provided to the rats of Group 2 or 3 (e.g., as by injection into the tail vein, or by oral gavage) inflammation is induced in all rats by a sub-plantar injection of a 1% carrageenin solution (50 μ l) into the right hind paw. Three hours after carrageenin administration paw thickness is measured as an indication of edema (e.g., swelling) and induced inflammatory response to the injected carrageenin solution.

Significant swelling is evident in untreated rats by three hours after carrageenin injection. Inflammation also is measured by histology by standard means, following euthanasia e.g.: the right hind paw from each animal is removed at the ankle joint and weighed and foot pad tissue is fixed in 10% neutral buffered formalin, and slides prepared for visual examination by staining the prepared tissue with hematoxylin and eosin.

The morphogen-treated rats show substantially reduced edema induction following carrageenin injection as compared with the untreated rats.

Example 13. Morphogen Treatment of Allergic
Encephalomyelitis

The following example demonstrates morphogen
5 efficacy in treating experimental allergic
encephalomyelitis (EAE) in a rat. EAE is a
well-characterized animal model for multiple sclerosis,
an autoimmune disease. A detailed description of the
protocol is disclosed in Kuruvilla, et al., (1991) PNAS
10 88:2918-2921, the disclosure of which is incorporated
herein by reference.

Briefly, EAE is induced in rats (e.g., Long-Evans,
Charles River Laboratories, Wilmington, MA) by
15 injection of a CNS tissue (e.g., spinal cord)
homogenate in complete Freund's adjuvant (CFA) on days
-44, -30 and 0 (last day of immunization), by
subcutaneous injection to three sites on the animal's
back. Morphogen is administered daily by
20 interperitoneal injection beginning on day -31.
Preferably, a series of morphogen dose ranges is
evaluated (e.g., low, medium and high) as for
Example 12, above.) Control rats receive morphogen
vehicle only (e.g. 0.9% NaCl or buffered saline). Rats
25 are examined daily for signs of disease and graded on
an increasing severity scale of 0-4.

In the absence of morphogen treatment, significant
neurological dysfunction (e.g., hind and fore limb
30 weakness, progressing to total hind limb paralysis) is
evident by day +7 to +10. Hematology, serum chemistry
profiles and histology are performed to evaluate the

- 92 -

degree of tissue necropsy using standard procedures. Morphogen treatment significantly inhibits the neurological dysfunction normally evident in an EAE animal. In addition, the histopathological markers typically associated with EAE are absent in the morphogen-treated animals.

Example 14. Morphogen Treatment of Collagen-Induced Arthritis

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The following example demonstrates the efficacy of morphogens in inhibiting the inflammatory response in a collagen-induced arthritis (CIA) in a rat. CIA is a well-characterized animal model for rheumatoid arthritis, an autoimmune disease. The protocol disclosed is essentially that disclosed in Kuruvilla et al., (1991) PNAS 88:2918-2921, incorporated by reference hereinabove. Briefly, CIA is induced in experimental rats (e.g., Long-Evans, Charles River Laboratories, Wilmington), by multiple intradermal injection of bovine Type II collagen (e.g., 100 μ g) in CFA (0.2 ml) on Day 1. Animals are divided into two groups: Group 1, control animals, which receive vehicle alone, and Group 2: morphogen-treated animals, which, preferably, are subdivided into low, medium and high dose ranges, as described for Example 13, above. Morphogen is administered daily (e.g., by tail vein injection) beginning at different times following collagen injection, e.g., beginning on day 7, 14, 28, 35 and 42. Animals are evaluated visually and paw thickness and body weight is monitored throughout the experiment. Animals are sacrificed on day 60 and the proximal and distal limb joints, and ear, tail and spinal cord prepared for histological evaluation as described for Examples 12 and 13, above. In a

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variation of the experiment, morphogen may be administered for prescribed periods, e.g., five day periods, beginning at different times following collagen injection (e.g., on days 0-4, 7-11, 14-18, 28-
5 32.)

In the absence of morphogen treatment, an arthritic condition typically is induced by 30 days post collagen injection. In morphogen-treated animals, CIA is
10 suppressed and the histopathological changes typically evidenced in control CIA-induced animals are absent: e.g., accumulations of activated mononuclear inflammatory cells and fibrous connective tissue. In addition, consistent with the results in Example 7,
15 above, serum anti-collagen antibody titers are suppressed significantly in the morphogen-treated animals.

20 Example 15. Screening Assay for Candidate Compounds which Alter Endogenous Morphogen Levels

Candidate compound(s) which may be administered to affect the level of a given morphogen may be found using the following screening assay, in which the level
25 of morphogen production by a cell type which produces measurable levels of the morphogen is determined with and without incubating the cell in culture with the compound, in order to assess the effects of the compound on the cell. This can be accomplished by
30 detection of the morphogen either at the protein or RNA level. A more detailed description also may be found in USSN 752,861, incorporated hereinabove by reference.

15.1 Growth of Cells in Culture

Cell cultures of kidney, adrenals, urinary bladder, brain, or other organs, may be prepared as described widely in the literature. For example, kidneys may be explanted from neonatal or new born or young or adult rodents (mouse or rat) and used in organ culture as whole or sliced (1-4 mm) tissues. Primary tissue cultures and established cell lines, also derived from kidney, adrenals, urinary, bladder, brain, mammary, or other tissues may be established in multiwell plates (6 well or 24 well) according to conventional cell culture techniques, and are cultured in the absence or presence of serum for a period of time (1-7 days). Cells may be cultured, for example, in Dulbecco's Modified Eagle medium (Gibco, Long Island, NY) containing serum (e.g., fetal calf serum at 1%-10%, Gibco) or in serum-deprived medium, as desired, or in defined medium (e.g., containing insulin, transferrin, glucose, albumin, or other growth factors).

Samples for testing the level of morphogen production includes culture supernatants or cell lysates, collected periodically and evaluated for OP-1 production by immunoblot analysis (Sambrook et al., eds., 1989, Molecular Cloning, Cold Spring Harbor Press, Cold Spring Harbor, NY), or a portion of the cell culture itself, collected periodically and used to prepare polyA⁺ RNA for RNA analysis. To monitor de novo OP-1 synthesis, some cultures are labeled according to conventional procedures with an ³⁵S-methionine/³⁵S-cysteine mixture for 6-24 hours and then evaluated to OP-1 synthesis by conventional immunoprecipitation methods.

15.2 Determination of Level of Morphogenic Protein

In order to quantitate the production of a morphogenic protein by a cell type, an immunoassay may be performed to detect the morphogen using a polyclonal or monoclonal antibody specific for that protein. For example, OP-1 may be detected using a polyclonal antibody specific for OP-1 in an ELISA, as follows.

10 1 µg/100 µl of affinity-purified polyclonal rabbit IgG specific for OP-1 is added to each well of a 96-well plate and incubated at 37°C for an hour. The wells are washed four times with 0.167M sodium borate buffer with 0.15 M NaCl (BSB), pH 8.2, containing 0.1% Tween 20. To minimize non-specific binding, the wells are blocked by filling completely with 1% bovine serum albumin (BSA) in BSB and incubating for 1 hour at 37°C. The wells are then washed four times with BSB containing 0.1% Tween 20. A 100 µl aliquot of an appropriate dilution of each of the test samples of cell culture supernatant is added to each well in triplicate and incubated at 37°C for 30 min. After incubation, 100 µl biotinylated rabbit anti-OP-1 serum (stock solution is about 1 mg/ml and diluted 1:400 in BSB containing 1% BSA before use) is added to each well and incubated at 37°C for 30 min. The wells are then washed four times with BSB containing 0.1% Tween 20. 100 µl streptavidin-alkaline (Southern Biotechnology Associates, Inc. Birmingham, Alabama, diluted 1:2000 in BSB containing 0.1% Tween 20 before use) is added to each well and incubated at 37°C for 30 min. The plates are washed four times with 0.5M Tris buffered Saline (TBS), pH 7.2. 50µl substrate (ELISA Amplification System Kit; Life Technologies, Inc., Bethesda, MD) is added to each well incubated at room temperature for 15

min. Then, 50 μ l amplifier (from the same amplification system kit) is added and incubated for another 15 min at room temperature. The reaction is stopped by the addition of 50 μ l 0.3 M sulphuric acid.

- 5 The OD at 490 nm of the solution in each well is recorded. To quantitate OP-1 in culture media, a OP-1 standard curve is performed in parallel with the test samples.

- 10 Polyclonal antibody may be prepared as follows. Each rabbit is given a primary immunization of 100 μ g/500 μ l E. coli produced OP-1 monomer (amino acids 328-431 in SEQ ID NO:5) in 0.1% SDS mixed with 500 μ l Complete Freund's Adjuvant. The antigen is injected
15 subcutaneously at multiple sites on the back and flanks of the animal. The rabbit is boosted after a month in the same manner using incomplete Freund's Adjuvant. Test bleeds are taken from the ear vein seven days later. Two additional boosts and test bleeds are
20 performed at monthly intervals until antibody against OP-1 is detected in the serum using an ELISA assay. Then, the rabbit is boosted monthly with 100 μ g of antigen and bled (15 ml per bleed) at days seven and ten after boosting.

25

- Monoclonal antibody specific for a given morphogen may be prepared as follows. A mouse is given two injections of E. coli produced OP-1 monomer. The first injection contains 100 μ g of OP-1 in complete Freund's
30 adjuvant and is given subcutaneously. The second injection contains 50 μ g of OP-1 in incomplete adjuvant and is given intraperitoneally. The mouse then receives a total of 230 μ g of OP-1 (amino acids 307-431 in SEQ ID NO:5) in four intraperitoneal injections at
35 various times over an eight month period. One week

prior to fusion, both mice are boosted intraperitoneally with 100 µg of OP-1 (307-431) and 30 µg of the N-terminal peptide (Ser₂₉₃-Asn₃₀₉-Cys) conjugated through the added cysteine to bovine serum albumin with SMCC crosslinking agent. This boost was repeated five days (IP), four days (IP), three days (IP) and one day (IV) prior to fusion. The mouse spleen cells are then fused to myeloma (e.g., 653) cells at a ratio of 1:1 using PEG 1500 (Boehringer Mannheim), and the cell fusion is plated and screened for OP-1-specific antibodies using OP-1 (307-431) as antigen. The cell fusion and monoclonal screening then are according to standard procedures well described in standard texts widely available in the art.

15

The invention may be embodied in other specific forms without departing from the spirit or essential characteristics thereof. The present embodiments are therefore to be considered in all respects as illustrative and not restrictive, the scope of the invention being indicated by the appended claims rather than by the foregoing description, and all changes which come within the meaning and range of equivalency of the claims are therefore intended to be embraced therein.

25

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT: KUBERASAMPATH, THANGAVEL
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15

(ii) TITLE OF INVENTION: MORPHOGEN-INDUCED MODULATION OF
INFLAMMATORY RESPONSE

(iii) NUMBER OF SEQUENCES: 33

(iv) CORRESPONDENCE ADDRESS:

20

(A) ADDRESSEE: CREATIVE BIOMOLECULES
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(E) COUNTRY: U.S.A.
25 (F) ZIP:

(v) COMPUTER READABLE FORM:

30

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Patent In Release #1.0, Version #1.25

(vii) PRIOR APPLICATION DATA:

35

(A) APPLICATION NUMBER: US 667,274
(B) FILING DATE: 11-MAR-1991

(vii) PRIOR APPLICATION DATA:

40

(A) APPLICATION NUMBER: US 753,059
(B) FILING DATE: 30-AUG-1991

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 752,764
(B) FILING DATE: 30-AUG-1991

(2) INFORMATION FOR SEQ ID NO:1:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acids
(C) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET

indicates one of the 20 naturally-occurring L-isomers, α -amino acids or a derivative thereof.

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120

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85

95

indicates one of the 20 naturally-occurring L-isomer, α -amino acids or a derivative thereof.

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SUBSTITUTE SHEET

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys
				55				60	
Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			65					70	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			75				80		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys
	85					90			
Xaa	Cys	Xaa							
95									

(2) INFORMATION FOR SEQ ID NO:3:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acids
(C) TOPOLOGY: linear
- 20 (ii) MOLECULE TYPE: protein
(ix) FEATURE:
(A) NAME: Generic Sequence 3
(D) OTHER INFORMATION: wherein each
Xaa is independently selected from
a group of one or more specified
amino acids as defined in the
specification.
- 25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

		Leu	Tyr	Val	Xaa	Phe			
		1				5			
30		Xaa	Xaa	Xaa	Gly	Trp	Xaa	Xaa	Trp Xaa
					10				
		Xaa	Ala	Pro	Gly	Xaa	Xaa	Xaa	Ala
		15				20			
35		Xaa	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa
			25						30
		Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	
					35				
		Xaa	Xaa	Xaa	Asn	His	Ala	Xaa	Xaa
40			40						45
		Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa
					50				
		Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys
			55					60	
45		Cys	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa
				65					
		Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	
		70					75		
		Xaa	Xaa	Xaa	Xaa	Val	Xaa	Leu	Xaa
				80					
50		Xaa	Xaa	Xaa	Xaa	Met	Xaa	Val	Xaa
		85					90		
		Xaa	Cys	Gly	Cys	Xaa			
				95					

SUBSTITUTE SHEET

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acids
 (C) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (ix) FEATURE:
 (A) NAME: Generic Sequence 4
 (D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Cys Xaa Xaa Xaa Xaa Leu Tyr Val Xaa Phe
 1 5 10
 Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
 15
 Xaa Ala Pro Xaa Gly Xaa Xaa Ala
 20 25
 Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
 25 30 35
 Xaa Pro Xaa Xaa Xaa Xaa Xaa
 40
 Asn Xaa Xaa Asn His Ala Xaa Xaa
 30 45 50
 Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa
 55
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 60 65
 Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
 35 70
 Xaa Xaa Xaa Leu Xaa Xaa Xaa
 75 80
 Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
 40 85
 Xaa Xaa Xaa Xaa Met Xaa Val Xaa
 90 95
 Xaa Cys Gly Cys Xaa
 100

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 amino acids
 (B) TYPE: amino acids
 (C) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (ix) FEATURE:
 (A) NAME: hOP-1 (mature form)

		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:							
5	Ser	Thr	Gly	Ser	Lys	Gln	Arg	Ser	Gln
	1				5				
	Asn	Arg	Ser	Lys	Thr	Pro	Lys	Asn	Gln
10	10					15			
	Glu	Ala	Leu	Arg	Met	Ala	Asn	Val	Ala
	20					25			
15	Glu	Asn	Ser	Ser	Ser	Asp	Gln	Arg	Gln
	30							35	
	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val
20	40								45
	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp
	50								
25	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala
	55					60			
	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
30	65					70			
	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala
	75							80	
35	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu
	85								90
	Val	His	Phe	Ile	Asn	Pro	Glu	Thr	Val
40	95								
	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln
	100					105			
45	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe
	110					115			
	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys
50	120							125	
	Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	Ala
	130								135
	Cys	Gly	Cys	His					

- 35 (2) INFORMATION FOR SEQ ID NO:6:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acids
- (C) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
- (A) NAME: mOP-1 (mature form)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

45	Ser	Thr	Gly	Gly	Lys	Gln	Arg	Ser	Gln
	1				5				
	Asn	Arg	Ser	Lys	Thr	Pro	Lys	Asn	Gln
50	10					15			
	Glu	Ala	Leu	Arg	Met	Ala	Ser	Val	Ala
	20					25			
	Glu	Asn	Ser	Ser	Ser	Asp	Gln	Arg	Gln
	30							35	

	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val
				40					45
	S r	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp
				50					
5	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala
	55					60			
	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
		65					70		
	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala
			75					80	
10	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu
			85						90
	Val	His	Phe	Ile	Asn	Pro	Asp	Thr	Val
				95					
15	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln
	100					105			
	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe
		110					115		
	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys
20			120					125	
	Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	Ala
			130						135
	Cys	Gly	Cys	His					

25 (2)

INFORMATION FOR SEQ ID NO:7:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 amino acids
 (B) TYPE: amino acids
 (C) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (ix) FEATURE:
 (A) NAME: hOP-2 (mature form)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

35	Ala	Val	Arg	Pro	Leu	Arg	Arg	Arg	Gln
	1				5				
	Pro	Lys	Lys	Ser	Asn	Glu	Leu	Pro	Gln
	10					15			
	Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp
40		20					25		
	Asp	Val	His	Gly	Ser	His	Gly	Arg	Gln
			30					35	
	Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
				40					45
45	Ser	Phe	Gln	Asp	Leu	Gly	Trp	Leu	Asp
				50					
	Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
	55					60			
	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser
		65					70		
50	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
			75					80	

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	Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
				85					90
	Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val
					95				
5	Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
	100					105			
	Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
		110					115		
	Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
			120					125	
10	Lys	His	Arg	Asn	Met	Val	Val	Lys	Ala
				130					135
	Cys	Gly	Cys	His					

15 (2) INFORMATION FOR SEQ ID NO:8:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 amino acids
 (B) TYPE: amino acids
 (C) TOPOLOGY: linear
 20 (ii) MOLECULE TYPE: protein
 (ix) FEATURE:
 (A) NAME: mOP-2 (mature form)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

25	Ala	Ala	Arg	Pro	Leu	Lys	Arg	Arg	Gln
	1				5				
	Pro	Lys	Lys	Thr	Asn	Glu	Leu	Pro	His
	10					15			
	Pro	Asn	Lys	Leu	Pro	Gly	Ile	Phe	Asp
		20					25		
30	Asp	Gly	His	Gly	Ser	Arg	Gly	Arg	Glu
			30					35	
	Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
				40					45
35	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Leu	Asp
				50					
	Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
	55					60			
	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
		65					70		
40	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
			75					80	
	Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
				85					90
45	Val	His	Leu	Met	Lys	Pro	Asp	Val	Val
					95				
	Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
	100					105			
	Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
		110					115		
50	Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
			120					125	

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Lys His Arg Asn Met Val Val Lys Ala
130 135
Cys Gly Cys His

5 (2)

INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: CBMP-2A(fx)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

15 Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser
1 5 10
Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro
15 20
Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu
20 25
Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser
35 40
Thr Asn His Ala Ile Val Gln Thr Leu Val Asn
45 50 55
25 Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys
60 65
Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu
70 75
Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys
30 80 85
Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly
90 95
Cys Arg
100

35

(2)

INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acids

40 (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: CBMP-2B(fx)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

45

Cys Arg Arg His Ser
1 5

Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn
10 15

50

Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala
20 25

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5 Phe Tyr Cys His Gly Asp Cys Pr Phe Pro Leu
30 35
Ala Asp His Leu Asn Ser Thr Asn His Ala Ile
40 45
Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser
50 55 60
Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu
65 70
Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Tyr
75 80
10 Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met
85 90
Val Val Glu Gly Cys Gly Cys Arg
95 100

15 (2) INFORMATION FOR SEQ ID NO:11:
20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 amino acids
(B) TYPE: amino acids
(C) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(ix) FEATURE:
(A) NAME: DPP(fx)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
25 Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser
1 5 10
Asp Val Gly Trp Asp Asp Trp Ile Val Ala Pro
15 20
30 Leu Gly Tyr Asp Ala Tyr Tyr Cys His Gly Lys
25 30
Cys Pro Phe Pro Leu Ala Asp His Phe Asn Ser
35 35 40
Thr Asn His Ala Val Val Gln Thr Leu Val Asn
45 50 55
Asn Asn Asn Pro Gly Lys Val Pro Lys Ala Cys
60 65
Cys Val Pro Thr Gln Leu Asp Ser Val Ala Met
70 75
40 Leu Tyr Leu Asn Asp Gln Ser Thr Val Val Leu
80 85
Lys Asn Tyr Gln Glu Met Thr Val Val Gly Cys
90 95
45 Gly Cys Arg
100

(2) INFORMATION FOR SEQ ID NO:12:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 amino acids
(B) TYPE: amino acids
(C) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
50

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(ix) FEATURE:

(A) NAME: Vgl(fx)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

5      Cys Lys Lys Arg His Leu Tyr Val Glu Phe Lys
      1          5          10
      Asp Val Gly Trp Gln Asn Trp Val Ile Ala Pro
      15          20
10     Gln Gly Tyr Met Ala Asn Tyr Cys Tyr Gly Glu
      25          30
      Cys Pro Tyr Pro Leu Thr Glu Ile Leu Asn Gly
      35          40
      Ser Asn His Ala Ile Leu Gln Thr Leu Val His
      45          50          55
15     Ser Ile Glu Pro Glu Asp Ile Pro Leu Pro Cys
      60          65
      Cys Val Pro Thr Lys Met Ser Pro Ile Ser Met
      70          75
      Leu Phe Tyr Asp Asn Asn Asp Asn Val Val Leu
      80          85
20     Arg His Tyr Glu Asn Met Ala Val Asp Glu Cys
      90          95
      Gly Cys Arg
      100

```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: Vgr-1(fx)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

35     Cys Lys Lys His Glu Leu Tyr Val Ser Phe Gln
      1          5          10
      Asp Val Gly Trp Gln Asp Trp Ile Ile Ala Pro
      15          20
40     Xaa Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu
      25          30
      Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala
      35          40
      Thr Asn His Ala Ile Val Gln Thr Leu Val His
      45          50          55
      Val Met Asn Pro Glu Tyr Val Pro Lys Pro Cys
      60          65
      Cys Ala Pro Thr Lys Val Asn Ala Ile Ser Val
      70          75

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Leu Tyr Ph Asp Asp Asn Ser Asn Val Ile Leu
80 85
Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys
90 95
5 Gly Cys His
100

(2) INFORMATION FOR SEQ ID NO:14:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 amino acids
(B) TYPE: protein
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
15 (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: human
(F) TISSUE TYPE: BRAIN
20

(ix) FEATURE:
(D) OTHER INFORMATION:
/product= "GDF-1 (fx)"

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly
1 5 10
30 Trp His Arg Trp Val Ile Ala Pro Arg Gly Phe Leu Ala Asn Tyr
15 20 25
Cys Gln Gly Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly
30 35 40
35 Gly Pro Pro Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His
45 50 55
Ala Ala Ala Pro Gly Ala Ala Asp Leu Pro Cys Cys Val Pro Ala
40 60 65 70
Arg Leu Ser Pro Ile Ser Val Leu Phe Phe Asp Asn Ser Asp Asn
75 80 85
45 Val Val Leu Arg Gln Tyr Glu Asp Met Val Val Asp Glu Cys Gly
90 95 100
Cys Arg
105

50

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys Xaa Xaa Xaa Xaa
1 5

15

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1822 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HOMO SAPIENS
(F) TISSUE TYPE: HIPPOCAMPUS

30

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 49..1341
(D) OTHER INFORMATION: /standard_name= "hOP1"

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTGC GGGGCC CGGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG 57
Met His Val
1

40

CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA 105
Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
5 10 15

45

CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC 153
Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
20 25 30 35

50

GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG 201
Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
40 45 50

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	CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC	249
	Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg	
	55 60 65	
5	CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG	297
	Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met	
	70 75 80	
10	CTG GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC	345
	Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly	
	85 90 95	
15	GGC CAG GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC	393
	Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly	
	100 105 110 115	
20	CCC CCT CTG GCC AGC CTG CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC	441
	Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp	
	120 125 130	
25	ATG GTC ATG AGC TTC GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC	489
	Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe	
	135 140 145	
30	CAC CCA CGC TAC CAC CAT CGA GAG TTC CGG TTT GAT CTT TCC AAG ATC	537
	His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile	
	150 155 160	
35	CCA GAA GGG GAA GCT GTC ACG GCA GCC GAA TTC CGG ATC TAC AAG GAC	585
	Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp	
	165 170 175	
40	TAC ATC CGG GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT	633
	Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr	
	180 185 190 195	
45	CAG GTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC	681
	Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu	
	200 205 210	
50	GAC AGC CGT ACC CTC TGG GCC TCG GAG GAG GGC TGG CTG GTG TTT GAC	729
	Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp	
	215 220 225	
55	ATC ACA GCC ACC AGC AAC CAC TGG GTG GTC AAT CCG CGG CAC AAC CTG	777
	Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu	
	230 235 240	
60	GGC CTG CAG CTC TCG GTG GAG ACG CTG GAT GGC CAG AGC ATC AAC CCC	825
	Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro	
	245 250 255	

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	AAG TTG GCG GGC CTG ATT GGG CGG CAC GGG CCC CAG AAC AAG CAG CCC Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro 260 265 270 275	873
5	TTC ATG GTG GCT TTC TTC AAG GCC ACG GAG GTC CAC TTC CGC AGC ATC Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile 280 285 290	921
10	CGG TCC ACG GGG AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG CCC Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro 295 300 305	969
15	AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC GTG GCA GAG AAC AGC AGC Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser 310 315 320	1017
20	AGC GAC CAG AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe 325 330 335	1065
	CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala 340 345 350 355	1113
25	GCC TAC TAC TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met 360 365 370	1161
30	AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn 375 380 385	1209
35	CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala 390 395 400	1257
40	ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys 405 410 415	1305
	TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His 420 425 430	1351
45	GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGGCCAG	1411
	GAACCAGCAG ACCAACTGCC TTTTGAGAGA CCTTCCCCTC CCTATCCCCA ACTTTAAAGG	1471
50	TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTTG ATCAGTTTTT CAGTGGCAGC	1531
	ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAACC TAGCAGGAAA AAAAAACAAC	1591

GCATAAAGAA AAATGGCCGG GCCAGGTCAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT 1651
CGTTTCCAGA GGTAATTATG AGCGCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG 1711
5 GCGGTGGCAA GGGGTGGGCA CATTGGTGTC TGTGCGAAAG GAAAATTGAC CCGGAAGTTC 1771
CTGTAATAAA TGTACAATA AAACGAATGA ATGAAAAAAAA AAAAAAAAAA A 1822

(2) INFORMATION FOR SEQ ID NO:17:

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 431 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15

- (ii) MOLECULE TYPE: protein

- (ix) FEATURE:

(D) OTHER INFORMATION: /Product="OPI-PP"

20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
1 5 10 15
25 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
20 25 30
30 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
35 40 45
Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
50 55 60
35 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
65 70 75 80
Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
85 90 95
40 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
100 105 110
45 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
115 120 125
Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
130 135 140
50 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
145 150 155 160

Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
165 170 175

5 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
180 185 190

Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
195 200 205

10 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
210 215 220

Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
225 230 235 240

15 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
245 250 255

Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
260 265 270

20 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
275 280 285

25 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
290 295 300

Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
305 310 315 320

30 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
325 330 335

Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
340 345 350

35 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
355 360 365

40 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
370 375 380

Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
385 390 395 400

45 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
405 410 415

Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
420 425 430

50

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(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1873 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: MURIDAE
 (F) TISSUE TYPE: EMBRYO

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 104..1393
 (D) OTHER INFORMATION: /note= "MOP1 (CDNA)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTGCAGCAAG TGACCTCGGG TCGTGGACCG CTGCCCTGCC CCCTCCGCTG CCACCTGGGG	60
CGGCGCGGGC CCGGTGCCCC GGATCGCGCG TAGAGCCGGC GCG ATG CAC GTG CGC	115
	Met His Val Arg
	1
TCG CTG CGC GCT GCG GCG CCA CAC AGC TTC GTG GCG CTC TGG GCG CCT	163
Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala Pro	
5 10 15 20	
CTG TTC TTG CTG CGC TCC GCC CTG GCC GAT TTC AGC CTG GAC AAC GAG	211
Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn Glu	
25 30 35	
GTG CAC TCC AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG CGG	259
Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg Arg	
40 45 50	
GAG ATG CAG CGG GAG ATC CTG TCC ATC TTA GGG TTG CCC CAT CGC CCG	307
Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro	
55 60 65	
CGC CCG CAC CTC CAG GGA AAG CAT AAT TCG GCG CCC ATG TTC ATG TTG	355
Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met Leu	
70 75 80	
GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG AGC GGG CCG GAC GGA CAG	403
Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Ser Gly Pro Asp Gly Gln	
85 90 95 100	

	GGC	TTC	TCC	TAC	CCC	TAC	AAG	GCC	GTC	TTC	AGT	ACC	CAG	GGC	CCC	CCT	451
	Gly	Phe	Ser	Tyr	Pro	Tyr	Lys	Ala	Val	Phe	Ser	Thr	Gln	Gly	Pro	Pro	
					105					110					115		
5	TTA	GCC	AGC	CTG	CAG	GAC	AGC	CAT	TTC	CTC	ACT	GAC	GCC	GAC	ATG	GTC	499
	Leu	Ala	Ser	Leu	Gln	Asp	Ser	His	Phe	Leu	Thr	Asp	Ala	Asp	Met	Val	
				120					125					130			
	ATG	AGC	TTC	GTC	AAC	CTA	GTG	GAA	CAT	GAC	AAA	GAA	TTC	TTC	CAC	CCT	547
10	Met	Ser	Phe	Val	Asn	Leu	Val	Glu	His	Asp	Lys	Glu	Phe	Phe	His	Pro	
			135					140					145				
	CGA	TAC	CAC	CAT	CGG	GAG	TTC	CGG	TTT	GAT	CTT	TCC	AAG	ATC	CCC	GAG	595
	Arg	Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu	Ser	Lys	Ile	Pro	Glu	
		150					155					160					
15	GGC	GAA	CGG	GTG	ACC	GCA	GCC	GAA	TTC	AGG	ATC	TAT	AAG	GAC	TAC	ATC	643
	Gly	Glu	Arg	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Asp	Tyr	Ile	
		165				170				175						180	
20	CGG	GAG	CGA	TTT	GAC	AAC	GAG	ACC	TTC	CAG	ATC	ACA	GTC	TAT	CAG	GTG	691
	Arg	Glu	Arg	Phe	Asp	Asn	Glu	Thr	Phe	Gln	Ile	Thr	Val	Tyr	Gln	Val	
					185					190					195		
	CTC	CAG	GAG	CAC	TCA	GGC	AGG	GAG	TCG	GAC	CTC	TTC	TTG	CTG	GAC	AGC	739
25	Leu	Gln	Glu	His	Ser	Gly	Arg	Glu	Ser	Asp	Leu	Phe	Leu	Leu	Asp	Ser	
				200					205					210			
	CGC	ACC	ATC	TGG	GCT	TCT	GAG	GAG	GGC	TGG	TTG	GTG	TTT	GAT	ATC	ACA	787
30	Arg	Thr	Ile	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Val	Phe	Asp	Ile	Thr	
			215					220					225				
	GCC	ACC	AGC	AAC	CAC	TGG	GTG	GTC	AAC	CCT	CGG	CAC	AAC	CTG	GGC	TTA	835
	Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	His	Asn	Leu	Gly	Leu	
		230					235					240					
35	CAG	CTC	TCT	GTG	GAG	ACC	CTG	GAT	GGG	CAG	AGC	ATC	AAC	CCC	AAG	TTG	883
	Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	Ile	Asn	Pro	Lys	Leu	
		245				250				255						260	
40	GCA	GGC	CTG	ATT	GGA	CGG	CAT	GGA	CCC	CAG	AAC	AAG	CAA	CCC	TTC	ATG	931
	Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	Lys	Gln	Pro	Phe	Met	
					265				270						275		
	GTG	GCC	TTC	TTC	AAG	GCC	ACG	GAA	GTC	CAT	CTC	CGT	AGT	ATC	CGG	TCC	979
45	Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Leu	Arg	Ser	Ile	Arg	Ser	
				280					285					290			
	ACG	GGG	GGC	AAG	CAG	CGC	AGC	CAG	AAT	CGC	TCC	AAG	ACG	CCA	AAG	AAC	1027
50	Thr	Gly	Gly	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	Lys	Thr	Pro	Lys	Asn	
			295					300					305				

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	CAA GAG GCC CTG AGG ATG GCC AGT GTG GCA GAA AAC AGC AGC AGT GAC	1075
	Gln Glu Ala Leu Arg Met Ala Ser Val Ala Glu Asn Ser Ser Ser Asp	
	310 315 320	
5	CAG AGG CAG GCC TGC AAG AAA CAT GAG CTG TAC GTC AGC TTC CGA GAC	1123
	Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp	
	325 330 335 340	
10	CTT GGC TGG CAG GAC TGG ATC ATT GCA CCT GAA GGC TAT GCT GCC TAC	1171
	Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr	
	345 350 355	
15	TAC TGT GAG GGA GAG TGC GCC TTC CCT CTG AAC TCC TAC ATG AAC GCC	1219
	Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala	
	360 365 370	
20	ACC AAC CAC GCC ATC GTC CAG ACA CTG GTT CAC TTC ATC AAC CCA GAC	1267
	Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Asp	
	375 380 385	
25	ACA GTA CCC AAG CCC TGC TGT GCG CCC ACC CAG CTC AAC GCC ATC TCT	1315
	Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser	
	390 395 400	
30	GTC CTC TAC TTC GAC GAC AGC TCT AAT GTC ATC CTG AAG AAG TAC AGA	1363
	Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg	
	405 410 415 420	
35	AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCTTCC TGAGACCCTG	1413
	Asn Met Val Val Arg Ala Cys Gly Cys His	
	425 430	
40	ACCTTTGCGG GGCCACACCT TTCCAAATCT TCGATGTCTC ACCATCTAAG TCTCTCACTG	1473
	CCCACCTTGG CGAGGAGAAC AGACCAACCT CTCCTGAGCC TTCCCTCACC TCCCAACCGG	1533
	AAGCATGTAA GGGTTCAGA AACCTGAGCG TGCAGCAGCT GATGAGCGCC CTTTCCTTCT	1593
	GGCACGTGAC GGACAAGATC CTACCAGCTA CCACAGCAAA CGCCTAAGAG CAGGAAAAAT	1653
	GTCTGCCAGG AAAGTGTTCA GTGTCCACAT GGCCCTTGGC GCTCTGAGTC TTTGAGGAGT	1713
	AATCGCAAGC CTCGTTTTCAGC TGCAGCAGAA GGAAGGGCTT AGCCAGGGTG GCGCTGGCG	1773
45	TCTGTGTTGA AGGGAAACCA AGCAGAAGCC ACTGTAATGA TATGTCACAA TAAAACCCAT	1833
	GAATGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAGAATTC	1873

(2) INFORMATION FOR SEQ ID NO:19:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 430 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
 (D) OTHER INFORMATION: /product= "mOP1-PP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

15 Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
 1 5 10 15
 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
 20 20 25 30
 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
 35 40 45
 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
 25 50 55 60
 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
 65 70 75 80
 30 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Ser Gly
 85 90 95
 Pro Asp Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr
 100 105 110
 35 Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp
 115 120 125
 Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu
 40 130 135 140
 Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser
 145 150 155 160
 45 Lys Ile Pro Glu Gly Glu Arg Val Thr Ala Ala Glu Phe Arg Ile Tyr
 165 170 175
 Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Gln Ile Thr
 180 185 190
 50 Val Tyr Gln Val Leu Gln Glu His Ser Gly Arg Glu Ser Asp Leu Phe
 195 200 205

Leu Leu Asp Ser Arg Thr Il Trp Ala Ser Glu Glu Gly Trp Leu Val
 210 215 220

5 Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His
 225 230 235 240

Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile
 245 250 255

10 Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys
 260 265 270

Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Leu Arg
 275 280 285

15 Ser Ile Arg Ser Thr Gly Gly Lys Gln Arg Ser Gln Asn Arg Ser Lys
 290 295 300

20 Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Ser Val Ala Glu Asn
 305 310 315 320

Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val
 325 330 335

25 Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly
 340 345 350

Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser
 355 360 365

30 Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe
 370 375 380

Ile Asn Pro Asp Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu
 385 390 395 400

Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu
 405 410 415

40 Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 420 425 430

(2) INFORMATION FOR SEQ ID NO:20:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1723 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
(F) TISSUE TYPE: HIPPOCAMPUS

5 (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 490..1696
(D) OTHER INFORMATION: /note= "hOP2 (cDNA)"

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

	GGCGCCGGCA GAGCAGGAGT GGCTGGAGGA GCTGTGGTTG GAGCAGGAGG TGGCACGGCA	60
	GGGCTGGAGG GCTCCCTATG AGTGGCGGAG ACGGCCCAGG AGGCGCTGGA GCAACAGCTC	120
15	CCACACCGCA CCAAGCGGTG GCTGCAGGAG CTCGCCCATC GCCCCTGCGC TGCTCGGACC	180
	GCGGCCACAG CCGGACTGGC GGGTACGGCG GCGACAGAGG CATTGGCCGA GAGTCCCAGT	240
20	CCGCAGAGTA GCGCCGGCCT CGAGGCGGTG GCGTCCCGGT CCTCTCCGTC CAGGAGCCAG	300
	GACAGGTGTC GCGCGGCGGG GCTCCAGGGA CCGCGCCTGA GGCCGGCTGC CCGCCCGTCC	360
	CGCCCCGCCC CGCCGCCCCG CGCCGCCCCA GCCCAGCCTC CTTGCCGTCG GGGCGTCCCC	420
25	AGGCCCTGGG TCGGCCGCGG AGCCGATGCG CGCCCGCTGA GCGCCCCAGC TGAGCGCCCC	480
	CGGCCTGCC ATG ACC GCG CTC CCC GGC CCG CTC TGG CTC CTG GGC CTG	528
	Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu	
30	1 5 10	
	GCG CTA TGC GCG CTG GGC GGG GGC GGC CCC GGC CTG CGA CCC CCG CCC	576
	Ala Leu Cys Ala Leu Gly Gly Gly Gly Pro Gly Leu Arg Pro Pro Pro	
	15 20 25	
35	GGC TGT CCC CAG CGA CGT CTG GGC GCG CGC GAG CGC CGG GAC GTG CAG	624
	Gly Cys Pro Gln Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Val Gln	
	30 35 40 45	
40	CGC GAG ATC CTG GCG GTG CTC GGG CTG CCT GGG CGG CCC CGG CCC CGC	672
	Arg Glu Ile Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg	
	50 55 60	
	GCG CCA CCC GCC GCC TCC CGG CTG CCC GCG TCC GCG CCG CTC TTC ATG	720
45	Ala Pro Pro Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met	
	65 70 75	
	CTG GAC CTG TAC CAC GCC ATG GCC GGC GAC GAC GAC GAG GAC GGC GCG	768
	Leu Asp Leu Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala	
50	80 85 90	

	CCC GCG GAG CGG CGC CTG GGC CGC GCC GAC CTG GTC ATG AGC TTC GTT	816
	Pro Ala Glu Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val	
	95 100 105	
5	AAC ATG GTG GAG CGA GAC CGT GCC CTG GGC CAC CAG GAG CCC CAT TGG	864
	Asn Met Val Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp	
	110 115 120 125	
10	AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC CCG GCT GGG GAG GCG GTC	912
	Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val	
	130 135 140	
15	ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG CCC AGC ATC CAC CTG CTC	960
	Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu	
	145 150 155	
20	AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG GTG GTC CAG GAG CAG TCC	1008
	Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser	
	160 165 170	
25	AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG ACG CTC CGA GCT	1056
	Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala	
	175 180 185	
30	GGA GAC GAG GGC TGG CTG GTG CTG GAT GTC ACA GCA GCC AGT GAC TGC	1104
	Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys	
	190 195 200 205	
35	TGG TTG CTG AAG CGT CAC AAG GAC CTG GGA CTC CGC CTC TAT GTG GAG	1152
	Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu	
	210 215 220	
40	ACT GAG GAC GGG CAC AGC GTG GAT CCT GGC CTG GCC GGC CTG CTG GGT	1200
	Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly	
	225 230 235	
45	CAA CGG GCC CCA CGC TCC CAA CAG CCT TTC GTG GTC ACT TTC TTC AGG	1248
	Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg	
	240 245 250	
50	GCC AGT CCG AGT CCC ATC CGC ACC CCT CGG GCA GTG AGG CCA CTG AGG	1296
	Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg	
	255 260 265	
55	AGG AGG CAG CCG AAG AAA AGC AAC GAG CTG CCG CAG GCC AAC CGA CTC	1344
	Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala Asn Arg Leu	
	270 275 280 285	
60	CCA GGG ATC TTT GAT GAC GTC CAC GGC TCC CAC GGC CGG CAG GTC TGC	1392
	Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly Arg Gln Val Cys	
	290 295 300	

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	CGT CGG CAC GAG CTC TAC GTC AGC TTC CAG GAC CTC GGC TGG CTG GAC	1440
	Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp	
	305 310 315	
5	TGG GTC ATC GCT CCC CAA GGC TAC TCG GCC TAT TAC TGT GAG GGG GAG	1488
	Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu	
	320 325 330	
10	TGC TCC TTC CCA CTG GAC TCC TGC ATG AAT GCC ACC AAC CAC GCC ATC	1536
	Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile	
	335 340 345	
15	CTG CAG TCC CTG GTG CAC CTG ATG AAG CCA AAC GCA GTC CCC AAG GCG	1584
	Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala	
	350 355 360 365	
20	TGC TGT GCA CCC ACC AAG CTG AGC GCC ACC TCT GTG CTC TAC TAT GAC	1632
	Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp	
	370 375 380	
25	AGC AGC AAC AAC GTC ATC CTG CGC AAA CAC CGC AAC ATG GTG GTC AAG	1680
	Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val Lys	
	385 390 395	
30	GCC TGC GGC TGC CAC T GAGTCAGCCC GCCCAGCCCT ACTGCAG	1723
	Ala Cys Gly Cys His	
	400	

(2) INFORMATION FOR SEQ ID NO:21:

(i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 402 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii)MOLECULE TYPE: protein

(ix)FEATURE:

(A)OTHER INFORMATION: /product= "hOP2-PP"

(xi)SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys
1 5 10 15
Ala Leu Gly Gly Gly Gly Pro Gly Leu Arg Pro Pro Pro Gly Cys Pro
20 25 30
Gln Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Val Gln Arg Glu Ile
35 40 45

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Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg Ala Pro Pro
 50 55 60
 5 Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu
 65 70 75 80
 Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala Pro Ala Glu
 85 90 95
 10 Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val Asn Met Val
 100 105 110
 Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp Lys Glu Phe
 115 120 125
 15 Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala
 130 135 140
 Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu Asn Arg Thr
 145 150 155 160
 20 Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser Asn Arg Glu
 165 170 175
 25 Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala Gly Asp Glu
 180 185 190
 Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys Trp Leu Leu
 195 200 205
 30 Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu Thr Glu Asp
 210 215 220
 Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly Gln Arg Ala
 225 230 235 240
 35 Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg Ala Ser Pro
 245 250 255
 40 Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg Arg Arg Gln
 260 265 270
 Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala Asn Arg Leu Pro Gly Ile
 275 280 285
 45 Phe Asp Asp Val His Gly Ser His Gly Arg Gln Val Cys Arg Arg His
 290 295 300
 Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp Val Ile
 305 310 315 320
 50

Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ser Phe
 325 330 335

Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser
 5 340 345 350

Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala Cys Cys Ala
 355 360 365

10 Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn
 370 375 380

Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val Lys Ala Cys Gly
 385 390 395 400

15 Cys His

(2) INFORMATION FOR SEQ ID NO:22:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1926 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: MURIDAE
 30 (F) TISSUE TYPE: EMBRYO
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 93..1289
 35 (D) OTHER INFORMATION: /note= "mOP2 cDNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCCAGGCACA GGTGCGCCGT CTGGTCTCTCC CCGTCTGGCG TCAGCCGAGC 50

40 CCGACCAGCT ACCAGTGGAT GCGCGCCGGC TGAAAGTCCG AG ATG GCT ATG CGT 104
 Met Ala Met Arg
 1

45 CCC GGG CCA CTC TGG CTA TTG GGC CTT GCT CTG TGC GCG CTG GGA GGC 152
 Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys Ala Leu Gly Gly
 5 10 15 20

GGC CAC GGT CCG CGT CCC CCG CAC ACC TGT CCC CAG CGT CGC CTG GGA 200
 50 Gly His Gly Pro Arg Pro Pro His Thr Cys Pro Gln Arg Arg Leu Gly
 25 30 35

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	GCG CGC GAG CGC CGC GAC ATG CAG CGT GAA ATC CTG GCG GTG CTC GGG	248
	Ala Arg Glu Arg Arg Asp Met Gln Arg Glu Ile Leu Ala Val Leu Gly	
	40 45 50	
5	CTA CCG GGA CGG CCC CGA CCC CGT GCA CAA CCC GCG GCT GCC CGG CAG	296
	Leu Pro Gly Arg Pro Arg Pro Arg Ala Gln Pro Ala Ala Arg Gln	
	55 60 65	
10	CCA GCG TCC GCG CCC CTC TTC ATG TTG GAC CTA TAC CAC GCC ATG ACC	344
	Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr His Ala Met Thr	
	70 75 80	
15	GAT GAC GAC GAC GGC GGG CCA CCA CAG GCT CAC TTA GGC CGT GCC GAC	392
	Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala His Leu Gly Arg Ala Asp	
	85 90 95 100	
20	CTG GTC ATG AGC TTC GTC AAC ATG GTG GAA CGC GAC CGT ACC CTG GGC	440
	Leu Val Met Ser Phe Val Asn Met Val Glu Arg Asp Arg Thr Leu Gly	
	105 110 115	
25	TAC CAG GAG CCA CAC TGG AAG GAA TTC CAC TTT GAC CTA ACC CAG ATC	488
	Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe Asp Leu Thr Gln Ile	
	120 125 130	
30	CCT GCT GGG GAG GCT GTC ACA GCT GCT GAG TTC CGG ATC TAC AAA GAA	536
	Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Glu	
	135 140 145	
35	CCC AGC ACC CAC CCG CTC AAC ACA ACC CTC CAC ATC AGC ATG TTC GAA	584
	Pro Ser Thr His Pro Leu Asn Thr Thr Leu His Ile Ser Met Phe Glu	
	150 155 160	
40	GTG GTC CAA GAG CAC TCC AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT	632
	Val Val Gln Glu His Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp	
	165 170 175 180	
45	CTT CAG ACG CTC CGA TCT GGG GAC GAG GGC TGG CTG GTG CTG GAC ATC	680
	Leu Gln Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu Val Leu Asp Ile	
	185 190 195	
50	ACA GCA GCC AGT GAC CGA TGG CTG CTG AAC CAT CAC AAG GAC CTG GGA	728
	Thr Ala Ala Ser Asp Arg Trp Leu Leu Asn His His Lys Asp Leu Gly	
	200 205 210	
55	CTC CGC CTC TAT GTG GAA ACC GCG GAT GGG CAC AGC ATG GAT CCT GGC	776
	Leu Arg Leu Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp Pro Gly	
	215 220 225	
60	CTG GCT GGT CTG CTT GGA CGA CAA GCA CCA CGC TCC AGA CAG CCT TTC	824
	Leu Ala Gly Leu Leu Gly Arg Gln Ala Pro Arg Ser Arg Gln Pro Phe	
	230 235 240	

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	ATG GTA ACC TTC TTC AGG GCC AGC CAG AGT CCT GTG CGG GCC CCT CGG	872
	Met Val Thr Phe Phe Arg Ala Ser Gln Ser Pro Val Arg Ala Pro Arg	
	245 250 255 260	
5	GCA GCG AGA CCA CTG AAG AGG AGG CAG CCA AAG AAA ACG AAC GAG CTT	920
	Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro Lys Lys Thr Asn Glu Leu	
	265 270 275	
10	CCG CAC CCC AAC AAA CTC CCA GGG ATC TTT GAT GAT GGC CAC GGT TCC	968
	Pro His Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser	
	280 285 290	
15	CGC GGC AGA GAG GTT TGC CGC AGG CAT GAG CTC TAC GTC AGC TTC CGT	1016
	Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Arg	
	295 300 305	
20	GAC CTT GGC TGG CTG GAC TGG GTC ATC GCC CCC CAG GGC TAC TCT GCC	1064
	Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala	
	310 315 320	
25	TAT TAC TGT GAG GGG GAG TGT GCT TTC CCA CTG GAC TCC TGT ATG AAC	1112
	Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys Met Asn	
	325 330 335 340	
30	GCC ACC AAC CAT GCC ATC TTG CAG TCT CTG GTG CAC CTG ATG AAG CCA	1160
	Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro	
	345 350 355	
35	GAT GTT GTC CCC AAG GCA TGC TGT GCA CCC ACC AAA CTG AGT GCC ACC	1208
	Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr	
	360 365 370	
40	TCT GTG CTG TAC TAT GAC AGC AGC AAC AAT GTC ATC CTG CGT AAA CAC	1256
	Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His	
	375 380 385	
45	CGT AAC ATG GTG GTC AAG GCC TGT GGC TGC CAC TGAGGCCCG CCCAGCATCC	1309
	Arg Asn Met Val Val Lys Ala Cys Gly Cys His	
	390 395	
50	TGCTTCTACT ACCTTACCAT CTGGCCGGGC CCCTCTCCAG AGGCAGAAAC CCTTCTATGT	1369
	TATCATAGCT CAGACAGGGG CAATGGGAGG CCCTTCACTT CCCCTGGCCA CTTCTGTCTA	1429
	AAATTCTGGT CTTTCCAGT TCCTCTGTCC TTCATGGGGT TTCGGGGCTA TCACCCCGCC	1489
	CTCTCCATCC TCCTACCCCA AGCATAGACT GAATGCACAC AGCATCCCAG AGCTATGCTA	1549
	ACTGAGAGGT CTGGGGTCAG CACTGAAGGC CCACATGAGG AAGACTGATC CTTGGCCATC	1609
	CTCAGCCCAC AATGGCAAAT TCTGGATGGT CTAAGAAGGC CGTGGAATTC TAAACTAGAT	1669

GATCTGGGCT CTCGACCA TTCATTGTGG CAGTTGGGAC ATTTTATAGGT ATAACAGACA 1729
 CATACTTA GATCAATGCA TCGCTGTACT CCTTGAAATC AGAGCTAGCT TGTTAGAAAA 1789
 5 AGAATCAGAG CCAGGTATAG CGGTGCATGT CATTAAATCCC AGCGCTAAAG AGACAGAGAC 1849
 AGGAGAATCT CTGTGAGTTC AAGGCCACAT AGAAAGAGCC TGTCTCGGGA GCAGGAAAAA 1909
 AAAAAAAAAAC GGAATTC 1926

10 (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 amino acids
 15 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20 (ix) FEATURE:
 (D) OTHER INFORMATION: /product= "mOP2-PP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

25 Met Ala Met Arg Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys
 1 5 10 15
 Ala Leu Gly Gly Gly His Gly Pro Arg Pro Pro His Thr Cys Pro Gln
 20 25 30
 30 Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Met Gln Arg Glu Ile Leu Ala
 35 40 45
 Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg Ala Gln Pro Ala Ala
 35 50 55 60 65
 Ala Arg Gln Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr His Ala
 70 75 80
 40 Met Thr Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala His Leu Gly Arg
 85 90 95
 Ala Asp Leu Val Met Ser Phe Val Asn Met Val Glu Arg Asp Arg Thr
 100 105 110
 45 Leu Gly Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe Asp Leu Thr
 115 120 125 130
 Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr
 135 140 145
 50

Lys Glu Pro Ser Thr His Pro Leu Asn Thr Thr Leu His Ile Ser Met
150 155 160

5 Phe Glu Val Val Gln Glu His Ser Asn Arg Glu Ser Asp Leu Phe Phe
165 170 175

Leu Asp Leu Gln Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu Val Leu
180 185 190

10 Asp Ile Thr Ala Ala Ser Asp Arg Trp Leu Leu Asn His His Lys Asp
195 200 205 210

Leu Gly Leu Arg Leu Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp
215 220 225

15 Pro Gly Leu Ala Gly Leu Leu Gly Arg Gln Ala Pro Arg Ser Arg Gln
230 235 240

20 Pro Phe Met Val Thr Phe Phe Arg Ala Ser Gln Ser Pro Val Arg Ala
245 250 255

Pro Arg Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro Lys Lys Thr Asn
260 265 270

25 Glu Leu Pro His Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His
275 280 285 290

Gly Ser Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Ser
295 300 305

30 Phe Arg Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr
310 315 320

Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys
325 330 335

Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met
340 345 350

40 Lys Pro Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser
355 360 365 370

Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg
375 380 385

45 Lys His Arg Asn Met Val Val Lys Ala Cys Gly Cys His
390 395

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(2) INFORMATION FOR SEQ ID NO:24:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..1368
(D) OTHER INFORMATION: /STANDARD NAME="60A"

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: WHARTON, KRISTI A.; THOMSEN, GERALD H.;
GELBERT, WILLIAM M.
(B) TITLE: DROSOPHILA 60A GENE...
(C) JOURNAL: PROC. NAT'L ACAD. SCI. USA
(D) VOLUME: 88
(E) RELEVANT RESIDUES IN SEQ ID NO:3: FROM 1 TO 1368
(F) PAGES: 9214-9218
(G) DATE: OCT - 1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATG TCG GGA CTG CGA AAC ACC TCG GAG GCC GTT GCA GTG CTC GCC TCC	48
Met Ser Gly Leu Arg Asn Thr Ser Glu Ala Val Ala Val Leu Ala Ser	
1 5 10 15	
CTG GGA CTC GGA ATG GTT CTG CTC ATG TTC GTG GCG ACC ACG CCG CCG	96
Leu Gly Leu Gly Met Val Leu Leu Met Phe Val Ala Thr Thr Pro Pro	
20 25 30	
GCC GTT GAG GCC ACC CAG TCG GGG ATT TAC ATA GAC AAC GGC AAG GAC	144
Ala Val Glu Ala Thr Gln Ser Gly Ile Tyr Ile Asp Asn Gly Lys Asp	
35 40 45	
CAG ACG ATC ATG CAC AGA GTG CTG AGC GAG GAC GAC AAG CTG GAC GTC	192
Gln Thr Ile Met His Arg Val Leu Ser Glu Asp Asp Lys Leu Asp Val	
50 55 60	
TCG TAC GAG ATC CTC GAG TTC CTG GGC ATC GCC GAA CGG CCG ACG CAC	240
Ser Tyr Glu Ile Leu Glu Phe Leu Gly Ile Ala Glu Arg Pro Thr His	
65 70 75 80	
CTG AGC AGC CAC CAG TTG TCG CTG AGG AAG TCG GCT CCC AAG TTC CTG	288
Leu Ser Ser His Gln Leu Ser Leu Arg Lys Ser Ala Pro Lys Phe Leu	
85 90 95	

	CTG GAC GTC TAC CAC CGC ATC ACG GCG GAG GAG GGT CTC AGC GAT CAG	336
	Leu Asp Val Tyr His Arg Ile Thr Ala Glu Glu Gly Leu Ser Asp Gln	
	100 105 110	
5	GAT GAG GAC GAC GAC TAC GAA CGC GGC CAT CGG TCC AGG AGG AGC GCC	384
	Asp Glu Asp Asp Asp Tyr Glu Arg Gly His Arg Ser Arg Arg Ser Ala	
	115 120 125	
10	GAC CTC GAG GAG GAT GAG GGC GAG CAG CAG AAG AAC TTC ATC ACC GAC	432
	Asp Leu Glu Glu Asp Glu Gly Glu Gln Gln Lys Asn Phe Ile Thr Asp	
	130 135 140	
15	CTG GAC AAG CGG GCC ATC GAC GAG AGC GAC ATC ATC ATG ACC TTC CTG	480
	Leu Asp Lys Arg Ala Ile Asp Glu Ser Asp Ile Ile Met Thr Phe Leu	
	145 150 155 160	
20	AAC AAG CGC CAC CAC AAT GTG GAC GAA CTG CGT CAC GAG CAC GGC CGT	528
	Asn Lys Arg His His Asn Val Asp Glu Leu Arg His Glu His Gly Arg	
	165 170 175	
25	CGC CTG TGG TTC GAC GTC TCC AAC GTG CCC AAC GAC AAC TAC CTG GTG	576
	Arg Leu Trp Phe Asp Val Ser Asn Val Pro Asn Asp Asn Tyr Leu Val	
	180 185 190	
30	ATG GCC GAG CTG CGC ATC TAT CAG AAC GCC AAC GAG GGC AAG TGG CTG	624
	Met Ala Glu Leu Arg Ile Tyr Gln Asn Ala Asn Glu Gly Lys Trp Leu	
	195 200 205	
35	ACC GCC AAC AGG GAG TTC ACC ATC ACG GTA TAC GCC ATT GGC ACC GGC	672
	Thr Ala Asn Arg Glu Phe Thr Ile Thr Val Tyr Ala Ile Gly Thr Gly	
	210 215 220	
40	ACG CTG GGC CAG CAC ACC ATG GAG CCG CTG TCC TCG GTG AAC ACC ACC	720
	Thr Leu Gly Gln His Thr Met Glu Pro Leu Ser Ser Val Asn Thr Thr	
	225 230 235 240	
45	GGG GAC TAC GTG GGC TGG TTG GAG CTC AAC GTG ACC GAG GGC CTG CAC	768
	Gly Asp Tyr Val Gly Trp Leu Glu Leu Asn Val Thr Glu Gly Leu His	
	245 250 255	
50	GAG TGG CTG GTC AAG TCG AAG GAC AAT CAT GGC ATC TAC ATT GGA GCA	816
	Glu Trp Leu Val Lys Ser Lys Asp Asn His Gly Ile Tyr Ile Gly Ala	
	260 265 270	
55	CAC GCT GTC AAC CGA CCC GAC CGC GAG GTG AAG CTG GAC GAC ATT GGA	864
	His Ala Val Asn Arg Pro Asp Arg Glu Val Lys Leu Asp Asp Ile Gly	
	275 280 285	
60	CTG ATC CAC CGC AAG GTG GAC GAC GAG TTC CAG CCC TTC ATG ATC GGC	912
	Leu Ile His Arg Lys Val Asp Asp Glu Phe Gln Pro Phe Met Ile Gly	
	290 295 300	

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	TTC TTC CGC GGA CCG GAG CTG ATC AAG GCG ACG GCC CAC AGC AGC CAC	960
	Phe Ph Arg Gly Pro Glu Leu Il Lys Ala Thr Ala His S r Ser His	
	305 310 315 320	
5	CAC AGG AGC AAG CGA AGC GCC AGC CAT CCA CGC AAG CGC AAG AAG TCG	1008
	His Arg Ser Lys Arg Ser Ala Ser His Pro Arg Lys Arg Lys Lys Ser	
	325 330 335	
10	GTG TCG CCC AAC AAC GTG CCG CTG CTG GAA CCG ATG GAG AGC ACG CGC	1056
	Val Ser Pro Asn Asn Val Pro Leu Leu Glu Pro Met Glu Ser Thr Arg	
	340 345 350	
15	AGC TGC CAG ATG CAG ACC CTG TAC ATA GAC TTC AAG GAT CTG GGC TGG	1104
	Ser Cys Gln Met Gln Thr Leu Tyr Ile Asp Phe Lys Asp Leu Gly Trp	
	355 360 365	
	CAT GAC TGG ATC ATC GCA CCA GAG GGC TAT GGC GCC TTC TAC TGC AGC	1152
	His Asp Trp Ile Ile Ala Pro Glu Gly Tyr Gly Ala Phe Tyr Cys Ser	
	370 375 380	
20	GGC GAG TGC AAT TTC CCG CTC AAT GCG CAC ATG AAC GCC ACG AAC CAT	1200
	Gly Glu Cys Asn Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His	
	385 390 395 400	
25	GCG ATC GTC CAG ACC CTG GTC CAC CTG CTG GAG CCC AAG AAG GTG CCC	1248
	Ala Ile Val Gln Thr Leu Val His Leu Leu Glu Pro Lys Lys Val Pro	
	405 410 415	
30	AAG CCC TGC TGC GCT CCG ACC AGG CTG GGA GCA CTA CCC GTT CTG TAC	1296
	Lys Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr	
	420 425 430	
35	CAC CTG AAC GAC GAG AAT GTG AAC CTG AAA AAG TAT AGA AAC ATG ATT	1344
	His Leu Asn Asp Glu Asn Val Asn Leu Lys Lys Tyr Arg Asn Met Ile	
	435 440 445	
	GTG AAA TCC TGC GGG TGC CAT TGA	1368
	Val Lys Ser Cys Gly Cys His	
	450 455	

(2) INFORMATION FOR SEQ ID NO:25:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 455 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

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	Met	Ser	Gly	Leu	Arg	Asn	Thr	Ser	Glu	Ala	Val	Ala	Val	Leu	Ala	Ser	
	1				5					10					15		
5	Leu	Gly	Leu	Gly	Met	Val	Leu	Leu	Met	Phe	Val	Ala	Thr	Thr	Pro	Pro	
				20					25					30			
	Ala	Val	Glu	Ala	Thr	Gln	Ser	Gly	Ile	Tyr	Ile	Asp	Asn	Gly	Lys	Asp	
				35				40					45				
10	Gln	Thr	Ile	Met	His	Arg	Val	Leu	Ser	Glu	Asp	Asp	Lys	Leu	Asp	Val	
		50					55						60				
	Ser	Tyr	Glu	Ile	Leu	Glu	Phe	Leu	Gly	Ile	Ala	Glu	Arg	Pro	Thr	His	
	65				70						75					80	
15	Leu	Ser	Ser	His	Gln	Leu	Ser	Leu	Arg	Lys	Ser	Ala	Pro	Lys	Phe	Leu	
					85					90					95		
	Leu	Asp	Val	Tyr	His	Arg	Ile	Thr	Ala	Glu	Glu	Gly	Leu	Ser	Asp	Gln	
20				100					105					110			
	Asp	Glu	Asp	Asp	Asp	Tyr	Glu	Arg	Gly	His	Arg	Ser	Arg	Arg	Ser	Ala	
			115					120					125				
25	Asp	Leu	Glu	Glu	Asp	Glu	Gly	Glu	Gln	Gln	Lys	Asn	Phe	Ile	Thr	Asp	
		130					135					140					
	Leu	Asp	Lys	Arg	Ala	Ile	Asp	Glu	Ser	Asp	Ile	Ile	Met	Thr	Phe	Leu	
	145					150					155					160	
30	Asn	Lys	Arg	His	His	Asn	Val	Asp	Glu	Leu	Arg	His	Glu	His	Gly	Arg	
					165					170					175		
	Arg	Leu	Trp	Phe	Asp	Val	Ser	Asn	Val	Pro	Asn	Asp	Asn	Tyr	Leu	Val	
35				180					185					190			
	Met	Ala	Glu	Leu	Arg	Ile	Tyr	Gln	Asn	Ala	Asn	Glu	Gly	Lys	Trp	Leu	
			195					200					205				
40	Thr	Ala	Asn	Arg	Glu	Phe	Thr	Ile	Thr	Val	Tyr	Ala	Ile	Gly	Thr	Gly	
		210					215					220					
	Thr	Leu	Gly	Gln	His	Thr	Met	Glu	Pro	Leu	Ser	Ser	Val	Asn	Thr	Thr	
	225					230					235					240	
45	Gly	Asp	Tyr	Val	Gly	Trp	Leu	Glu	Leu	Asn	Val	Thr	Glu	Gly	Leu	His	
					245					250					255		
	Glu	Trp	Leu	Val	Lys	Ser	Lys	Asp	Asn	His	Gly	Ile	Tyr	Ile	Gly	Ala	
50				260					265					270			

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His Ala Val Asn Arg Pro Asp Arg Glu Val Lys Leu Asp Asp Ile Gly
 275 280 285
 5 Leu Ile His Arg Lys Val Asp Asp Glu Phe Gln Pro Phe Met Ile Gly
 290 295 300
 Phe Phe Arg Gly Pro Glu Leu Ile Lys Ala Thr Ala His Ser Ser His
 305 310 315 320
 10 His Arg Ser Lys Arg Ser Ala Ser His Pro Arg Lys Arg Lys Lys Ser
 325 330 335
 Val Ser Pro Asn Asn Val Pro Leu Leu Glu Pro Met Glu Ser Thr Arg
 340 345 350
 15 Ser Cys Gln Met Gln Thr Leu Tyr Ile Asp Phe Lys Asp Leu Gly Trp
 355 360 365
 20 His Asp Trp Ile Ile Ala Pro Glu Gly Tyr Gly Ala Phe Tyr Cys Ser
 370 375 380
 Gly Glu Cys Asn Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His
 385 390 395 400
 25 Ala Ile Val Gln Thr Leu Val His Leu Leu Glu Pro Lys Lys Val Pro
 405 410 415
 Lys Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr
 420 425 430
 30 His Leu Asn Asp Glu Asn Val Asn Leu Lys Lys Tyr Arg Asn Met Ile
 435 440 445
 35 Val Lys Ser Cys Gly Cys His
 450 455

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..102
 (D) OTHER INFORMATION: /note="BMP3"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

(i)SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii)MOLECULE TYPE: protein

(ix)FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: /note="BMP3"

(xi)SEQUENCE DESCRIPTION: SEQ ID NO:26:

Cys Ala Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp Ser
 1 5 10 15
 Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala Tyr Try Cys Ser Gly
 20 25 30
 Ala Cys Gln Phe Pro Met Pro Lys Ser Leu Lys Pro Ser Asn His Ala
 25 35 40 45
 Thr Ile Gln Ser Ile Val Ala Arg Ala Val Gly Val Val Pro Gly Ile
 50 55 60
 Pro Glu Pro Cys Cys Val Pro Glu Lys Met Ser Ser Leu Ser Ile Leu
 30 65 70 75 80
 Phe Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met
 35 85 90 95
 Thr Val Glu Ser Cys Ala Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HOMO SAPIENS

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /note= "BMP5"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
 1 5 10 15
 10 Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly
 20 25 30
 15 Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 35 40 45
 Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys
 50 55 60
 20 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80
 Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 85 90 95
 25 Arg Ser Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:28:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

35

- (ii) MOLECULE TYPE: protein

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: HOMO SAPIENS

40

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /note= "BMP6"

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Cys Arg Lys His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln
 50 1 5 10 15

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Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly
20 25 30
5 Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
35 40 45
Ile Val Gln Thr Leu Val His Leu Met Asn Pro Glu Tyr Val Pro Lys
50 55 60
10 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
65 70 75 80
Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Trp Met Val Val
85 90 95
15 Arg Ala Cys Gly Cys His
100

(2) INFORMATION FOR SEQ ID NO:29:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
25 (ii) MOLECULE TYPE: protein
(ix) FEATURE:
(A) NAME/KEY: Protein
30 (B) LOCATION: 1..102
(D) OTHER INFORMATION: /label= OPX
/note= "WHEREIN XAA AT EACH POS'N IS INDEPENDENTLY
SELECTED FROM THE RESIDUES OCCURRING AT THE
CORRESPONDING POS'N IN THE C-TERMINAL SEQUENCE OF MOUSE
35 OR HUMAN OP1 OR OP2 (SEE SEQ. ID NOS. 5,6,7 and 8 or
16,18,20 and 22.)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

40 Cys Xaa Xaa His Glu Leu Tyr Val Xaa Phe Xaa Asp Leu Gly Trp Xaa
1 5 10 15
Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
20 25 30
45 Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
35 40 45
Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
50 50 55 60

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Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
65 70 75 80
5 Asp Xaa Ser Xaa Asn Val Xaa Leu Xaa Lys Xaa Arg Asn Met Val Val
85 90 95
Xaa Ala Cys Gly Cys His
100

10 (2) INFORMATION FOR SEQ ID NO:30:

- (i)SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acids
(C) TOPOLOGY: linear
15 (ii)MOLECULE TYPE: protein
(ix)FEATURE:
(A) NAME: Generic Sequence 5
(D) OTHER INFORMATION: wherein each Xaa is independently
20 selected from a group of one or more specified amino acids as
defined in the specification.

(xi)SEQUENCE DESCRIPTION: SEQ ID NO:30:

25 Leu Xaa Xaa Xaa Phe
1 5
Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
10
Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala
15 20
30 Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
25 30
Xaa Pro Xaa Xaa Xaa Xaa Xaa
35
Xaa Xaa Xaa Asn His Ala Xaa Xaa
40 45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
40 55 60
Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
65
Xaa Xaa Xaa Leu Xaa Xaa Xaa
70 75
45 Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
80
Xaa Xaa Xaa Xaa Met Xaa Val Xaa
85 90
Xaa Cys Xaa Cys Xaa
50 95

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(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 102 amino acids
(B) TYPE: amino acids
(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- 10 (A) NAME: Generic Sequence 6
(D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

15 Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe
1 5 10
Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
15
20 Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala
20 25
Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
30 35
Xaa Pro Xaa Xaa Xaa Xaa Xaa
25 40
Xaa Xaa Xaa Asn His Ala Xaa Xaa
45 50
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
55
30 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
60 65
Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
70
Xaa Xaa Xaa Leu Xaa Xaa Xaa
35 75 80
Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
85
Xaa Xaa Xaa Xaa Met Xaa Val Xaa
90 95
40 Xaa Cys Xaa Cys Xaa
100

(2) INFORMATION FOR SEQ ID NO:32:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1238 base pairs, 372 amino acids
(B) TYPE: nucleic acid, amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 50 (ii) MOLECULE TYPE: cDNA

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(iii) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (F) TISSUE TYPE: BRAIN

5 (iv) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION:
 (D) OTHER INFORMATION:
 /product= "GDF-1"
 /note= "GDF-1 CDNA"

10

(x) PUBLICATION INFORMATION:
 (A) AUTHORS: Lee, Se-Jin
 (B) TITLE: Expression of Growth/Differentiation Factor 1
 (C) JOURNAL: Proc. Nat'l Acad. Sci.
 (D) VOLUME: 88
 (E) RELEVANT RESIDUES: 1-1238
 (F) PAGES: 4250-4254
 (G) DATE: May-1991
 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGGGACACCG GCCCGCCCT CAGCCCACTG GTCCCGGGCC GCCGCGGACC CTGCGCACTC 60
 TCTGGTCATC GCCTGGGAGG AAG ATG CCA CCG CCG CAG CAA GGT CCC TGC GGC 113
 25 Met Pro Pro Pro Gln Gln Gly Pro Cys Gly
 1 5 10

CAC CAC CTC CTC CTC CTC CTG GCC CTG CTG CTG CCC TCG CTG CCC 158
 His His Leu Leu Leu Leu Leu Ala Leu Leu Leu Pro Ser Leu Pro
 15 20 25

30 CTG ACC CGC GCC CCC GTG CCC CCA GGC CCA GCC GCC GCC CTG CTC 203
 Leu Thr Arg Ala Pro Val Pro Pro Gly Pro Ala Ala Ala Leu Leu
 30 35 40

35 CAG GCT CTA GGA CTG CGC GAT GAG CCC CAG GGT GCC CCC AGG CTC 248
 Gln Ala Leu Gly Leu Arg Asp Glu Pro Gln Gly Ala Pro Arg Leu
 45 50 55

40 CGG CCG GTT CCC CCG GTC ATG TGG CGC CTG TTT CGA CGC CGG GAC 293
 Arg Pro Val Pro Pro Val Met Trp Arg Leu Phe Arg Arg Arg Asp
 60 65 70

45 CCC CAG GAG ACC AGG TCT GGC TCG CGG CGG ACG TCC CCA GGG GTC 338
 Pro Gln Glu Thr Arg Ser Gly Ser Arg Arg Thr Ser Pro Gly Val
 75 80 85

ACC CTG CAA CCG TGC CAC GTG GAG GAG CTG GGG GTC GCC GGA AAC 383
 Thr Leu Gln Pro Cys His Val Glu Glu Leu Gly Val Ala Gly Asn
 90 95 100

50

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	ATC GTG CGC CAC ATC CCG GAC CGC GGT GCG CCC ACC CGG GCC TCG	428
	Ile Val Arg His Ile Pro Asp Arg Gly Ala Pro Thr Arg Ala Ser	
	105 110 115	
5	GAG CCT GTC TCG GCC GCG GGG CAT TGC CCT GAG TGG ACA GTC GTC	473
	Glu Pro Val Ser Ala Ala Gly His Cys Pro Glu Trp Thr Val Val	
	120 125 130	
10	TTC GAC CTG TCG GCT GTG GAA CCC GCT GAG CGC CCG AGC CGG GCC	518
	Phe Asp Leu Ser Ala Val Glu Pro Ala Glu Arg Pro Ser Arg Ala	
	135 140 145	
15	CGC CTG GAG CTG CGT TTC GCG GCG GCG GCG GCG GCA GCC CCG GAG	563
	Arg Leu Glu Leu Arg Phe Ala Ala Ala Ala Ala Ala Pro Glu	
	150 155 160	
20	GGC GGC TGG GAG CTG AGC GTG GCG CAA GCG GGC CAG GGC GCG GGC	608
	Gly Gly Trp Glu Leu Ser Val Ala Gln Ala Gly Gln Gly Ala Gly	
	165 170 175	
25	GCG GAC CCC GGG CCG GTG CTG CTC CGC CAG TTG GTG CCC GCC CTG	653
	Ala Asp Pro Gly Pro Val Leu Leu Arg Gln Leu Val Pro Ala Leu	
	180 185 190	
30	GGG CCG CCA GTG CGC GCG GAG CTG CTG GGC GCC GCT TGG GCT CGC	698
	Gly Pro Pro Val Arg Ala Glu Leu Leu Gly Ala Ala Trp Ala Arg	
	195 200 205	
35	AAC GCC TCA TGG CCG CGC AGC CTC CGC CTG GCG CTG GCG CTA CGC	743
	Asn Ala Ser Trp Pro Arg Ser Leu Arg Leu Ala Leu Ala Leu Arg	
	210 215 220	
40	CCC CGG GCC CCT GCC GCC TGC GCG CGC CTG GCC GAG GCC TCG CTG	788
	Pro Arg Ala Pro Ala Ala Cys Ala Arg Leu Ala Glu Ala Ser Leu	
	225 230 235	
45	CTG CTG GTG ACC CTC GAC CCG CGC CTG TGC CAC CCC CTG GCC CGG	833
	Leu Leu Val Thr Leu Asp Pro Arg Leu Cys His Pro Leu Ala Arg	
	240 245 250	
50	CCG CGG CGC GAC GCC GAA CCC GTG TTG GGC GGC GGC CCC GGG GGC	878
	Pro Arg Arg Asp Ala Glu Pro Val Leu Gly Gly Gly Pro Gly Gly	
	255 260 265	
55	GCT TGT CGC GCG CGG CGG CTG TAC GTG AGC TTC CGC CAG GTG GGC	923
	Ala Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly	
	270 275 280	
60	TGG CAC CGC TGG GTC ATC GCG CCG CGC CCC TTC CTG GCC AAC TAC	968
	Trp His Arg Trp Val Ile Arg Pro Arg Gly Phe Leu Ala Asn Tyr	
	285 290 295	

TGC CAG GGT CAG TGC GCG CTG CCC GTC GCG CTG TCG GGG TCC GGG 1013
 Cys Gln Gly Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly
 300 305 310
 5 GGG CCG CCG GCG CTC AAC CAC GCT GTG CTG CGC GCG CTC ATG CAC 1058
 Gly Pro Pro Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His
 315 320 325
 10 GCG GCC GCC CCG GGA GCC GCC GAC CTG CCC TGC TGC GTG CCC GCG 1103
 Ala Ala Ala Pro Gly Ala Ala Asp Leu Pro Cys Cys Val Pro Ala
 330 335 340
 15 CGC CTG TCG CCC ATC TCC GTG CTC TTC TTT GAC AAC AGC GAC AAC 1148
 Arg Leu Ser Pro Ile Ser Val Leu Phe Phe Asp Asn Ser Asp Asn
 345 350 355
 GTG GTG CTG CGG CAG TAT GAG GAC ATG GTG GTG GAC GAG TGC GGC 1193
 Val Val Leu Arg Gln Tyr Glu Asp Met Val Val Asp Glu Cys Gly
 360 365 370
 20 TGC CGC TAACCCGGGG CGGGCAGGGA CCCGGGCCCA ACAATAAATG CCGCGTGG 1238
 Cys Arg
 372

25 (2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 372 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: human
 - (F) TISSUE TYPE: BRAIN
- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION:
 - (D) OTHER INFORMATION: /function=
/product= "GDF-1"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Pro Pro Pro Gln Gln Gly Pro Cys Gly
 1 5 10

	His His Leu Leu Leu Leu Leu Ala Leu Leu Leu Pro Ser Leu Pro	15	20	25
5	Leu Thr Arg Ala Pro Val Pro Pro Gly Pro Ala Ala Ala Leu Leu	30	35	40
	Gln Ala Leu Gly Leu Arg Asp Glu Pro Gln Gly Ala Pro Arg Leu	45	50	55
10	Arg Pro Val Pro Pro Val Met Trp Arg Leu Phe Arg Arg Arg Asp	60	65	70
	Pro Gln Glu Thr Arg Ser Gly Ser Arg Arg Thr Ser Pro Gly Val	75	80	85
15	Thr Leu Gln Pro Cyc His Val Glu Glu Leu Gly Val Ala Gly Asn	90	95	100
	Ile Val Arg His Ile Pro Asp Arg Gly Ala Pro Thr Arg Ala Ser	105	110	115
20	Glu Pro Val Ser Ala Ala Gly His Cys Pro Glu Trp Thr Val Val	120	125	130
	Phe Asp Leu Ser Ala Val Glu Pro Ala Glu Arg Pro Ser Arg Ala	135	140	145
	Arg Leu Glu Leu Arg Phe Ala Ala Ala Ala Ala Ala Ala Pro Glu	150	155	160
30	Gly Gly Trp Glu Leu Ser Val Ala Gln Ala Gly Gln Gly Ala Gly	165	170	175
	Ala Asp Pro Gly Pro Val Leu Leu Arg Gln Leu Val Pro Ala Leu	180	185	190
35	Gly Pro Pro Val Arg Ala Glu Leu Leu Gly Ala Ala Trp Ala Arg	195	200	205
40	Asn Ala Ser Trp Pro Arg Ser Leu Arg Leu Ala Leu Ala Leu Arg	210	215	220
	Pro Arg Ala Pro Ala Ala Cys Ala Arg Leu Ala Glu Ala Ser Leu	225	230	235
45	Leu Leu Val Thr Leu Asp Pro Arg Leu Cys His Pro Leu Ala Arg	240	245	250
	Pro Arg Arg Asp Ala Glu Pro Val Leu Gly Gly Gly Pro Gly Gly	255	260	265
50				

	Ala Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly	270	275	280
5	Trp His Arg Trp Val Ile Arg Pro Arg Gly Ph Leu Ala Asn Tyr	285	290	295
	Cys Gln Gly Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly	300	305	310
10	Gly Pro Pro Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His	315	320	325
	Ala Ala Ala Pro Gly Ala Ala Asp Leu Pro Cys Cys Val Pro Ala	330	335	340
15	Arg Leu Ser Pro Ile Ser Val Leu Phe Phe Asp Asn Ser Asp Asn	345	350	355
20	Val Val Leu Arg Gln Tyr Glu Asp Met Val Val Asp Glu Cys Gly	360	365	370
	Cys Arg	372		

SUBSTITUTE SHEET

What is claimed is:

1. A method for alleviating the tissue destructive effects associated with the inflammatory response to tissue injury in a mammal, the method comprising the step of:

providing to the injured tissue a therapeutically effective concentration of a morphogen sufficient to substantially inhibit or reduce the tissue damage resulting from said inflammatory response.
2. The method of claim 1 where said step of providing a therapeutically effective morphogen concentration to said injured tissue comprises the step of administering a therapeutically effective concentration of a morphogen to said mammal.
3. The method of claim 1 where said step of providing a therapeutically effective morphogen concentration to said injured tissue comprises the step of administering to said mammal an agent that stimulates in vivo a therapeutically effective concentration of an endogenous morphogen.
4. The method of claim 1 wherein said step of providing a therapeutically effective concentration of a morphogen is conducted prior to reduction or interruption of blood flow to the tissue.

5. The method of claim 1 wherein said step of providing a therapeutically effective concentration of a morphogen is conducted after reduction or interruption of blood flow to the tissue and before reperfusion.
6. The method of claim 1 wherein said step of administering a therapeutically effective amount of a morphogen is conducted following ischemia-reperfusion injury.
7. The method of claim 1 wherein said said step of administering a therapeutically effective amount of a morphogen is conducted following hyperoxia injury.
8. The method of claim 1 wherein said morphogen is provided to said tissue prior to said tissue injury.
9. The method of claim 1 wherein said step of providing a therapeutically effective concentration of a morphogen is conducted prior to ischemia-reperfusion injury.
10. The method of claim 1 wherein said tissue damage results from an abnormal immune response in said mammal.
11. The method of claim 1 wherein said tissue damage is associated with an inflammatory disease.
12. The method of claim 11 wherein said inflammatory disease is an autoimmune disease.

13. The method of claim 11 wherein said inflammatory disease comprises arthritis, psoriasis, dermatitis or diabetes.
14. The method of claim 13 wherein said arthritis is rheumatoid, degenerative or psoriatic arthritis.
15. The method of claim 11 wherein said inflammatory disease comprises an airway inflammation in a mammal.
16. The method of claim 15 wherein said airway inflammation comprises chronic bronchitis, emphysema, idiopathic pulmonary fibrosis or asthma.
17. The method of claim 11 wherein inflammatory disease comprises a generalized acute inflammatory response.
18. The method of claim 17 wherein said inflammatory disease comprises adult respiratory distress syndrome.
19. The method of claim 1 wherein said tissue damage is to a transplanted organ or tissue.
20. A method for reducing tissue damage associated with ischemia-reperfusion injury in a human, the method comprising the step of:

providing to the injured tissue a therapeutic concentration of a morphogen sufficient to alleviate the damage associated with said injury.

21. A method for reducing the tissue damage associated with hyperoxia injury in a human, the method comprising the step of:

providing to the injured tissue a therapeutic concentration of a morphogen sufficient to alleviate the damage associated with said injury.

22. The method of claim 20 or 21 wherein said step of providing a therapeutically effective morphogen concentration to said injured tissue comprises the step of administering a therapeutically effective concentration of a morphogen to said mammal.

23. The method of claim 20 or 21 wherein said step of providing a therapeutically effective morphogen concentration to said injured tissue comprises the step of administering to said mammal an agent that stimulates in vivo a therapeutically effective concentration of an endogenous morphogen.

24. The method of claim 1, 20 or 21 wherein said tissue is lung tissue, cardiac tissue, hepatic tissue or renal tissue.

25. The method of claim 6, 9 or 20 wherein said ischemic-reperfusion injury results from cardiac arrest, preliminary occlusion, arterial occlusion, coronary occlusion or occlusive stroke.

26. The method of claim 1, 20 or 21 wherein said morphogen comprises an amino acid sequence sharing at least 70% homology with one of the sequences selected from the group consisting of: OP-1, OP-2, CBMP2, Vgl(fx), Vgr(fx), DPP(fx), GDF-1(fx) and 60A(fx).
27. The method of claim 26 wherein said morphogen comprises an amino acid sequence sharing a last 80% homology with one of the sequences selected from the group consisting of: OP-1, OP-2, CBMP2, BMP3(fx), BMP5(fx), BMP6(fx), Vgl(fx), Vgr(fx), DPP(fx), GDF-1(fx) and 60A(fx).
28. The method of claim 1, 20 or 21 wherein said morphogen comprises an amino acid sequence having greater than 60% amino acid identity with the sequence defined by residues 43-139 of Seq. ID No. 5 (hOP1).
29. The method of claim 28 wherein said morphogen comprises an amino acid sequence having greater than 65% amino acid identity with the sequence defined by residues 43-139 of Seq. ID No. 5 (hOP1).
30. The method of claim 29 wherein said morphogen comprises an amino acid sequence defined by residues 43-139 of Seq. ID No. 5 (hOP1), including allelic and species variants thereof.
31. The method of claim 1, 20 or 21 wherein said morphogen comprises an amino acid sequence defined by Generic Sequences 1, 2, 3, 4, 5 or 6 (Seq. ID Nos. 1, 2, 3, 4, 30 or 31).

32. The method of claim 1, 20 or 21 where in said morphogen comprises an amino acid sequence defined by OPX (Seq. ID No. 29).
33. A method for reducing the ischemic-reperfusion injury associated with the interruption of blood flow to an organ in a clinical procedure, the method comprising the step of providing a therapeutic concentration of a morphogen to said organ prior to the interruption of blood flow.
34. A method for reducing the tissue injury associated with the reduction or interruption of blood flow to an organ or tissue in a clinical procedure, the method comprising the step of providing a therapeutic concentration of a morphogen to said organ or tissue after the reduction or interruption of blood flow to said organ or tissue.
35. The method of claim 33 or 34 wherein said clinical procedure is a carotid enterectomy, a coronary artery bypass, a tissue grafting procedure, an organ transplant, or a fibrinolytic therapy.
36. The method of claim 1, 33 or 34 wherein said morphogen is administered parenterally.
37. The method of claim 1, 33 or 34 wherein said morphogen is administered prophylactically.

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38. A pharmaceutical composition for use in alleviating the injury associated with tissue exposure to toxic oxygen concentrations comprising a therapeutically effective amount of a morphogen in admixture with a free oxygen radical inhibiting agent or an anticoagulant.
39. A pharmaceutical composition for topical administration comprising a therapeutically effective concentration of a morphogen in admixture with a dermatologically acceptable carrier.
40. A pharmaceutical composition for topical administration to a tissue comprising a therapeutically effective concentration of a morphogen dispersed in a biocompatible, non-irritating tissue surface adhesive.
41. The composition of claim 40 wherein said adhesive comprises hydroxypropylcellulose.
42. The composition of claim 38, 39 or 40 wherein said morphogen comprises an amino acid sequence sharing at least 70% homology with one of the sequences selected from the group consisting of: OP-1, OP-2, CBMP2, Vgl(fx), Vgr(fx), DPP(fx), GDF-1(fx) and 60A(fx).
43. The composition of claim 42 wherein said morphogen comprises an amino acid sequence sharing at least 80% homology with one of the sequences selected from the group consisting of: OP-1, OP-2, CBMP2, BMP3(fx), BMP5(fx), BMP6(fx), Vgl(fx), Vgr(fx), DPP(fx), GDF-1(fx) and 60A(fx).

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44. The composition of claim 38, 39 or 40 wherein said morphogen comprises an amino acid sequence having greater than 60% amino acid identity with the sequence defined by residues 43-139 of Seq. ID No. 5 (hOP1).
45. The composition of claim 44 wherein said morphogen comprises an amino acid sequence having greater than 65% amino acid identity with the sequence defined by residues 43-139 of Seq. ID No. 5 (hOP1).
46. The method of claim 45 wherein said morphogen comprises an amino acid sequence defined by residues 43-139 of Seq. ID No. 5 (hOP1), including allelic and species variants thereof.
47. The composition of claim 38, 39 or 40 wherein said morphogen comprises an amino acid sequence defined by Generic Sequences 1, 2, 3, 4, 5 or 6 (Seq. ID Nos. 1, 2, 3, 4, 30 or 31).
48. The composition of claim 38, 39 or 40 wherein said morphogen comprises an amino acid sequence defined by OPX (Seq. ID No. 29).
49. A method of enhancing the viability of an organ or tissue to be transplanted in a mammal, the method of comprising the step of:
- providing a therapeutically effective concentration of a morphogen to said tissue or organ to be transplanted.

50. The method of claim 49 wherein said therapeutically effective concentration is sufficient to substantially inhibit reperfusion injury to said tissue or organ.
51. The method of claim 49 wherein said morphogen is provided to said tissue or organ prior to reperfusion injury.
52. The method of claim 49 wherein said morphogen is provided to said tissue or organ prior to removal of said tissue or organ from the donor.
53. The method of claim 49 wherein said organ is placed in an organ preservation solution containing said morphogen or a morphogen-stimulating agent after removal of said organ from the donor and prior to transplantation in the recipient.
54. The method of claim 49 wherein said organ is selected from the group consisting of lung, heart, kidney, liver or pancreas.
55. The method of claim 49 wherein said living tissue comprises skin, bone marrow or gastrointestinal mucosa tissue.

56. A method for protecting a living tissue or transplant organ from the tissue destructive effects associated with the inflammatory response in a mammal, the method comprising the step of:

providing to said tissue or organ a therapeutically effective concentration of a morphogen.

57. A method of protecting a living tissue or transplanted organ from ischemia-reperfusion injury in a mammal, the method comprising the step of:

providing to said tissue or organ a therapeutically effective concentration of a morphogen, said concentration being sufficient to substantially inhibit or reduce the tissue damage associated with ischemia-reperfusion injury.

58. The method of claim 49, 56 or 57 wherein said step of providing a therapeutically effective morphogen concentration to said injured tissue comprises the step of administering a therapeutically effective concentration of a morphogen to said mammal.

59. The method of claim 49, 56 or 57 wherein said step of providing a therapeutically effective morphogen concentration to said injured tissue comprises the step of administering to said mammal an agent that stimulates in vivo a therapeutically effective concentration of an endogenous morphogen.

60. A composition useful as a living cell or living tissue preservation solution comprising:
- a fluid formulation having as osmotic pressure substantially equivalent to the osmotic pressure of living mammalian cells in admixture with
- a therapeutically effective concentration of a morphogen or morphogen-stimulating agent, said concentration being sufficient to protect living cell or tissue from the tissue destructive effects associated with the inflammatory response in a mammal when exposed to said cells or tissue.
61. The preservation solution of claim 60 wherein said therapeutically effective concentration is sufficient to substantially inhibit or reduce the tissue damage associated with ischemia-reperfusion injury.
62. The preservation solution of claim 60 wherein said formulation further comprises a sugar.
63. The preservation solution of claim 60 wherein said formulation further comprises an anticoagulant or a free oxygen radical inhibiting agent.
64. The invention of claim 49, 56, 57 or 60 wherein said morphogen comprises an amino acid sequence having greater than 60% amino acid identity with the sequence defined by residues 43-139 of Seq. ID No. 5 (hOP1).

65. A composition useful in a treatment method to alleviate tissue damage associated with the inflammatory response in a mammal, the composition comprising a therapeutically effective concentration of a morphogen or morphogen-stimulating agent.
66. The composition of claim 65 wherein said tissue damage is associated with ischemia-reperfusion injury or hyperoxia injury.
67. The composition of claim 65 wherein said tissue damage is to lung, cardiac, renal or hepatic tissue.
68. The composition of claim 65 wherein said tissue damage is to a transplanted organ or tissue.

AMENDED CLAIMS

[received by the International Bureau
on 10 February 1993 (10.02.93);
original claims 46 and 49 amended;
remaining claims unchanged (1 page)]

44. The composition of claim 38, 39 or 40 wherein said morphogen comprises an amino acid sequence having greater than 60% amino acid identity with the sequence defined by residues 43-139 of Seq. ID No. 5 (hOP1).
45. The composition of claim 44 wherein said morphogen comprises an amino acid sequence having greater than 65% amino acid identity with the sequence defined by residues 43-139 of Seq. ID No. 5 (hOP1).
46. The composition of claim 45 wherein said morphogen comprises an amino acid sequence defined by residues 43-139 of Seq. ID No. 5 (hOP1), including allelic and species variants thereof.
47. The composition of claim 38, 39 or 40 wherein said morphogen comprises an amino acid sequence defined by Generic Sequences 1, 2, 3, 4, 5 or 6 (Seq. ID Nos. 1, 2, 3, 4, 30 or 31).
48. The composition of claim 38, 39 or 40 wherein said morphogen comprises an amino acid sequence defined by OPX (Seq. ID No. 29).
49. A method of enhancing the viability of an organ or tissue to be transplanted in a mammal, the method comprising the step of:

providing a therapeutically effective concentration of a morphogen to said tissue or organ to be transplanted.

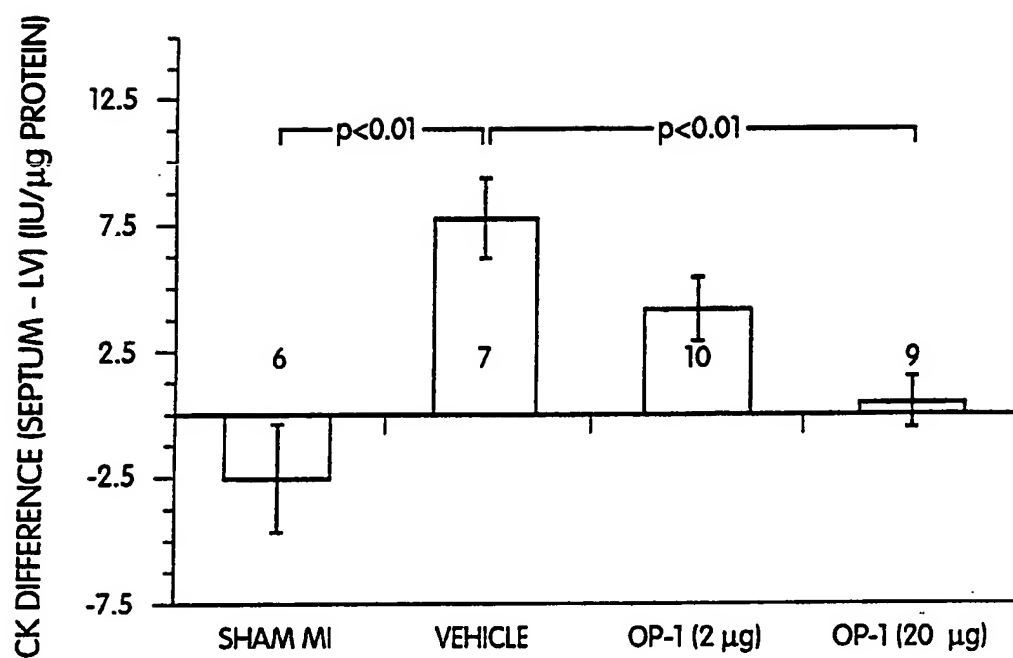


Fig. 1

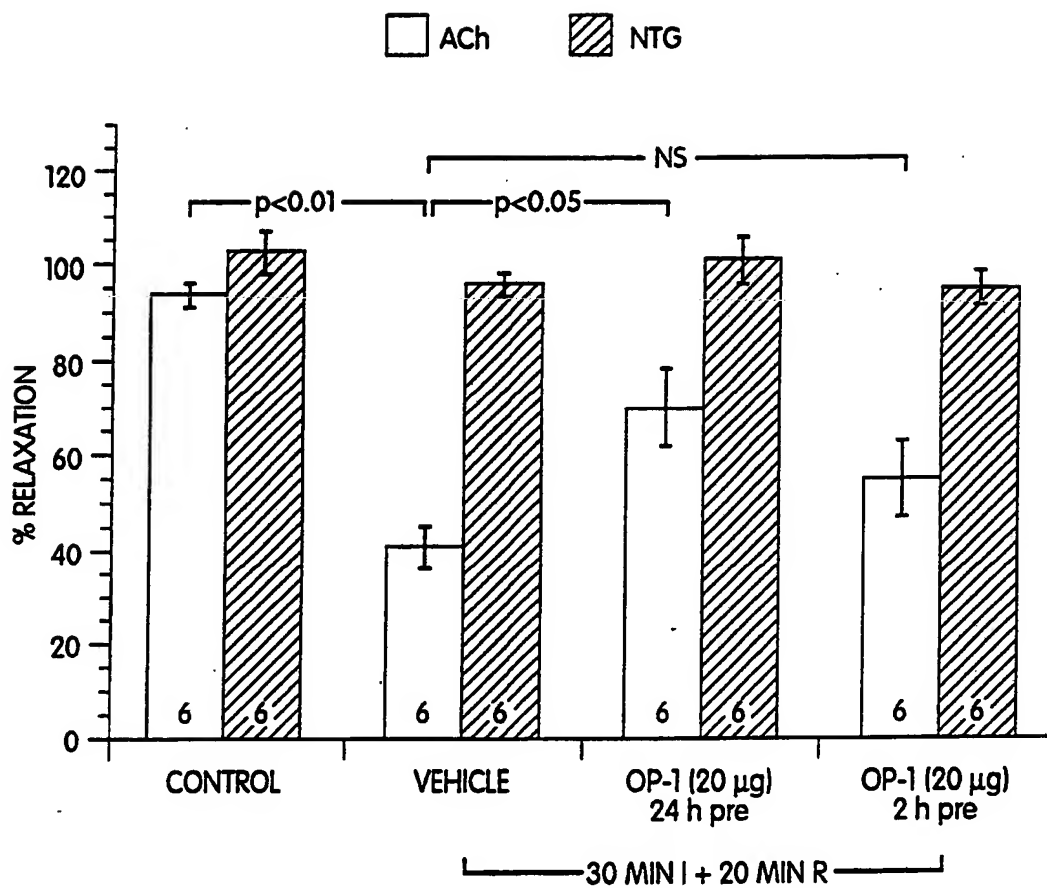


Fig 2

SUBSTITUTE SHEET

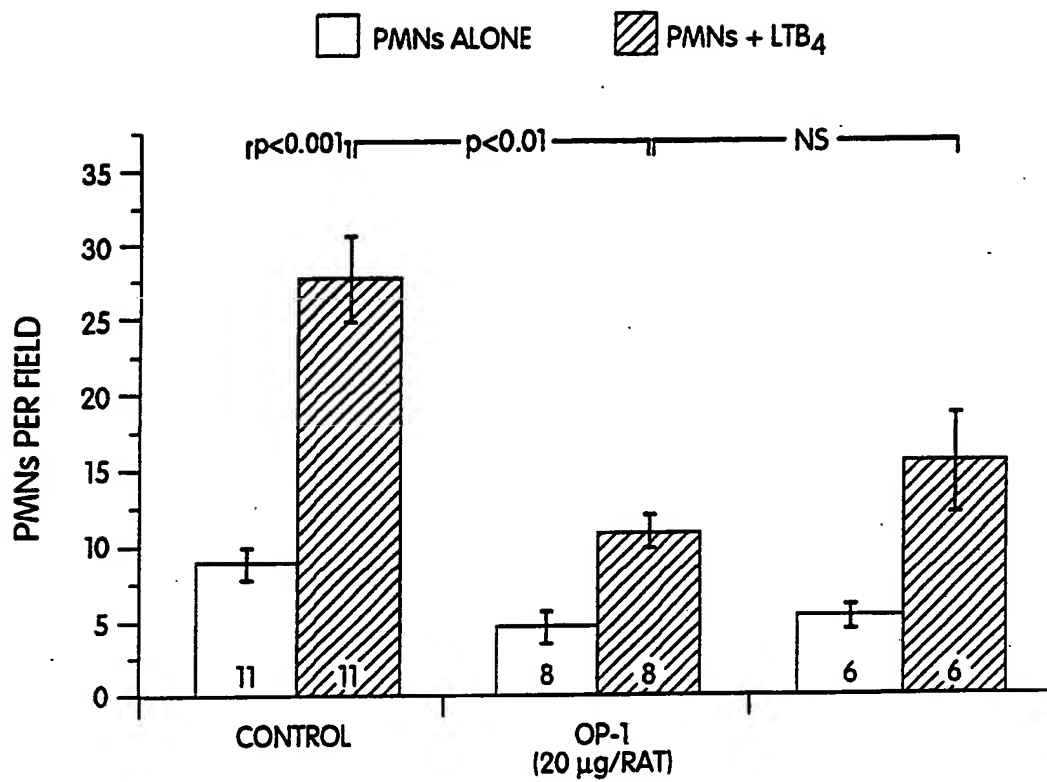


Fig. 3

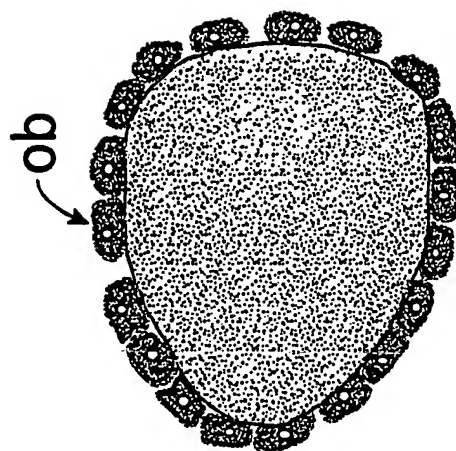


Fig. 4B

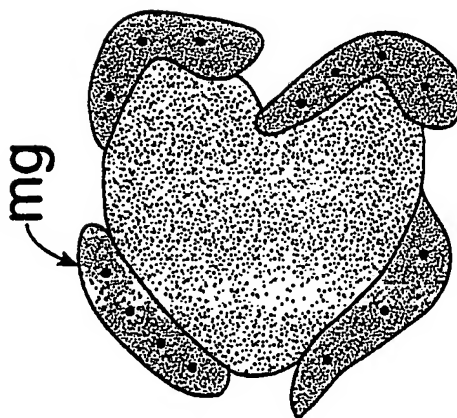


Fig. 4A

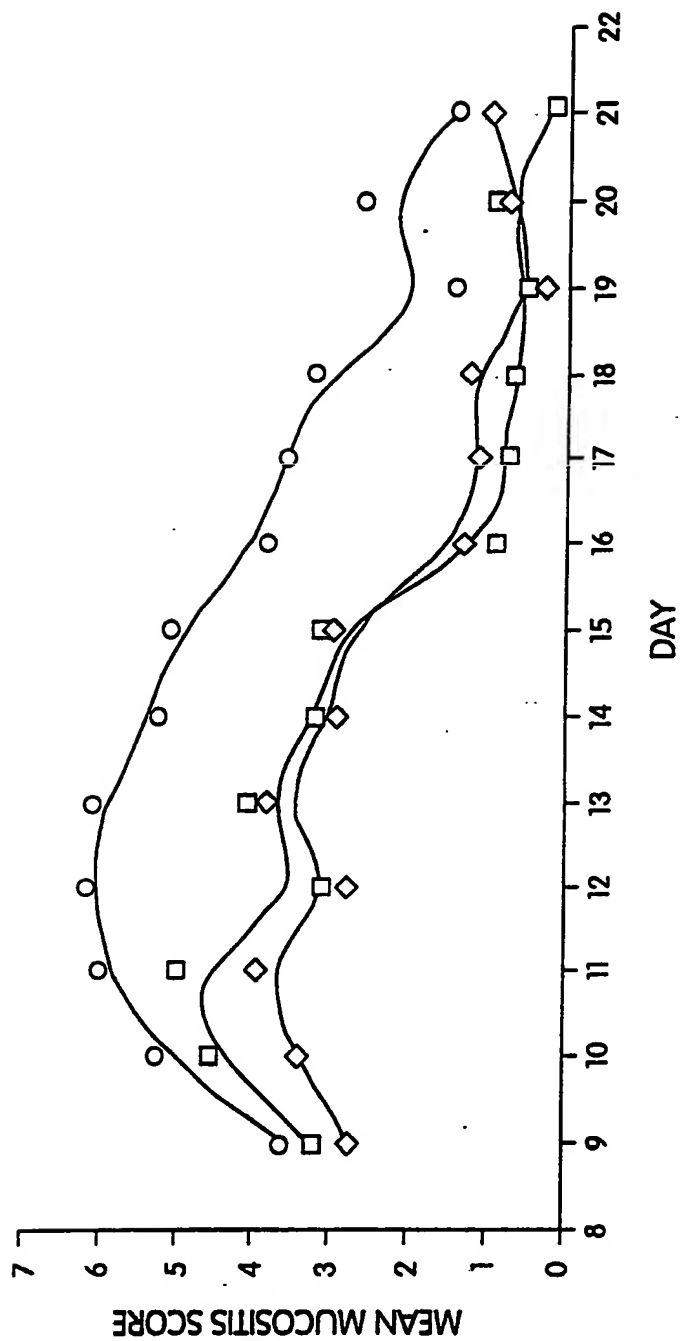


Fig. 5

Fig. 6A

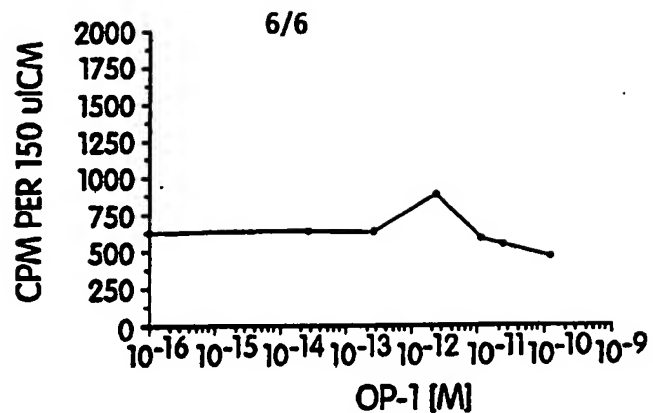


Fig. 6B

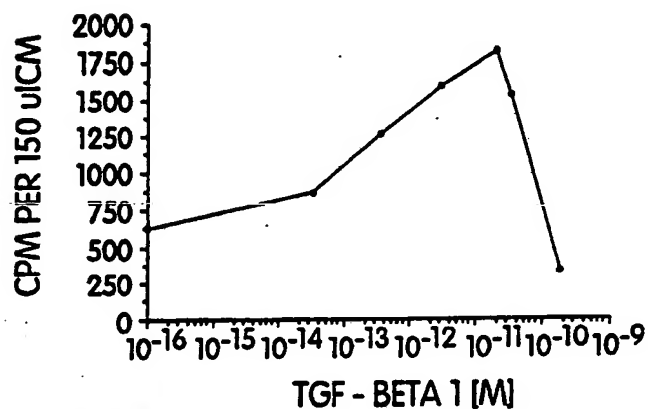


Fig. 6C

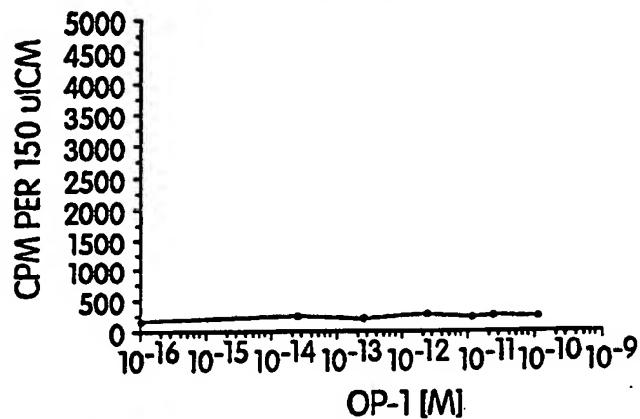
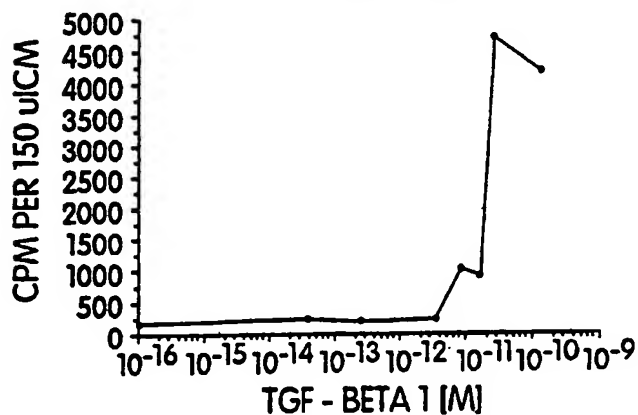


Fig. 6D



INTERNATIONAL SEARCH REPORT

PCT/US 92/07358

International Application No

I. CLASSIFICATION OF SUBJECT MATTER (If several classification symbols apply, indicate all)⁶

According to International Patent Classification (IPC) or to both National Classification and IPC

Int.Cl. 5 A61K37/02; A01N1/02

II. FIELDS SEARCHEDMinimum Documentation Searched⁷

Classification System	Classification Symbols
Int.Cl. 5	A61K ; C07K

Documentation Searched other than Minimum Documentation
to the extent that such Documents are Included in the Fields Searched⁸**III. DOCUMENTS CONSIDERED TO BE RELEVANT⁹**

Category ¹⁰	Citation of Document, ¹¹ with indication, where appropriate, of the relevant passages ¹²	Relevant to Claim No. ¹³
X	SCIENCE vol. 249, no. 4964, 6 July 1990, LANCASTER, PA US pages 61 - 64 LEFER A.M. ET AL 'Mediation of cardioprotection by Transforming growth factor-beta' cited in the application see the whole document ---	1-2, 4-9, 20-22, 25, 33-37, 57-58, 65-68
X	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA. vol. 88, no. 7, April 1991, WASHINGTON US pages 2918 - 2921 KURUVILLA, A.P. 'Protective effect of transforming growth factor beta1 on experimental autoimmune diseases in mice' cited in the application see the whole document ---	1-2, 10-19, 36-37, 56, 58, 65
	---	---

¹⁰ Special categories of cited documents: ¹⁰

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

¹¹ later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention¹² document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step¹³ document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.¹⁴ document member of the same patent family**IV. CERTIFICATION**

Date of the Actual Completion of the International Search

19 NOVEMBER 1992

Date of Mailing of this International Search Report

19.12.92

International Searching Authority

EUR PEAN PATENT FFICE

Signature of Authorized Officer

FERNANDEZ Y BRA F.

III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)		
Category *	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claims No.
X	EP,A,0 269 408 (GENENTECH INC.) 1 June 1988 see the whole document	1-2, 10-19, 36-37, 56,58,65
X	WO,A,9 000 900 (AMGEN INC.) 8 February 1990 see the whole document	1-2, 10-19, 36-37, 56,58,65
E	WO,A,9 215 323 (CREATIVE BIOMOLECULES) 17 September 1992 see page 6, line 1 - page 7, line 27 see page 77 - page 119	1-6, 8-12, 15-17, 20- 22-37, 56-59, 64-67
X	WO,A,9 105 802 (CREATIVE BIOMOLECULES) 2 May 1991 see page 20, line 19 - line 31 see page 59 - page 80	1-2, 10-13, 26-32, 36-37,65
X,P	WO,A,9 207 073 (CREATIVE BIOMOLECULES) 30 April 1992 see page 11, line 3 - line 15 see page 41 - page 60	1-2, 10-13, 26-29, 31-32, 36-37,65
X	WO,A,8 909 788 (CREATIVE BIOMOLECULES) 19 October 1989 cited in the application see page 6 - page 15	1-2, 10-13, 26-29, 31-32, 36-37,65
A	EMBO JOURNAL vol. 9, no. 7, 1990, EYNSHAM, OXFORD GB pages 2085 - 2093 ÖZKAYNAK, E. ET AL 'OP-1 cDNA encodes an osteogenic protein in the TGF-beta family' see the whole document	1-68

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 92/07358

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
see annex
2. ☒ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such
an extent that no meaningful international search can be carried out, specifically:
see annex
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all
searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment
of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report
covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is
restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/210

Remark: Although claims 1-37, 49-52 (partially, when the method is carried out in vivo), 54-57 (partially, when the method is carried out in vivo), 58 - 59, 64 (partially, according to the method of claims 49, 56 or 57) are directed to a method of treatment of the human or animal body the search has been carried out and based on the alleged effects of the composition.

OBSCURITIES, INCONSISTENCIES, CONTRADICTIONS, LACK OF CONCISENESS; LACK OF READY COMPREHENSIBILITY)

(ART. 6 PCT)

REASON:

1. Claim 46 has been understood as being dependant of claim 45. Therefore claim 46 should read: "The composition of claim 45, wherein said morphogen comprises an amino acid sequence defined by residues 43-139 of Seq. ID No. 5 (hOPI), including allelic and species variants thereof.
2. In view of the extremely large number of compounds used in the methods and compositions of claims 26-29, 31 (in as far as seq. ID 1 to 4 and 30-31), 42-45, 47 (in as far as seq. ID 1 to 4 and 30-31), 64, the search division considers that it is not economically reasonable to draw up a search report for the methods using, or the compositions comprising all the compounds defined in the claims. The search has therefore been limited, on the basis of the examples and claims, to the methods using, or the compositions comprising the seq. ID no. 5 to 29, 32 and 33 (Art. 17 (2) (a)(ii) and (b) PCT.
3. The term "morphogen" is not concise.

Therefor, and for the same reasons as given in paragraph 2 above, it has been understood as being one of the proteins defines in seq. ID 5 to 29, 32 or 33.
(Art. 6 PCT and Art. 17/2)(a)(ii) and (b) PCT)

**ANNEX TO THE INTERNATIONAL SEARCH REPORT
ON INTERNATIONAL PATENT APPLICATION NO.**

**US 9207358
SA 64364**

This annex lists the patent family members relating to the patent documents cited in the above-mentioned international search report. The members are as contained in the European Patent Office EDP file on
The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information. 19/11/92

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
EP-A-0269408	01-06-88	JP-A- 63211234	02-09-88
WO-A-9000900	08-02-90	AU-A- 4056089	19-02-90
WO-A-9215323	17-09-92	None	
WO-A-9105802	02-05-91	AU-A- 6648190	16-05-91
		CA-A- 2042577	18-04-91
		EP-A- 0448704	02-10-91
		JP-T- 4502336	23-04-92
		CA-A- 2027259	18-04-91
WO-A-9207073	30-04-92	AU-A- 8900091	20-05-92
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		US-A- 5011691	30-04-91
		AU-B- 628050	10-09-92
		AU-A- 3444989	03-11-89
		AU-B- 618357	19-12-91
		AU-A- 3530589	03-11-89
		EP-A- 0372031	13-06-90
		EP-A- 0362367	11-04-90
		JP-T- 3500655	14-02-91
		JP-T- 3502579	13-06-91
		WO-A- 8909787	19-10-89
		US-A- 5108753	28-04-92
		AU-B- 627850	03-09-92
		AU-A- 5174790	26-09-90
		EP-A- 0411105	06-02-91
		JP-T- 3504736	17-10-91
		WO-A- 9010018	07-09-90
		US-A- 4975526	04-12-90

EP FORM 1007